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Listing first 45 summaries
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Copyright (c) 1993 - 2005 Compugen Ltd.
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AGENCOURT	UI-R-EPO-	DG2-93n7	K-EST0196	UI-R-DY1-	AGENCOURT	0009b06.x	BY755449	UI-R-FSO-	387409 MA	DKFZp686E	AGENCOURT	602311010	N112 SSH-	602268114	UI-E-EJ0-	EST6973 h	UI-E-EJ0-	BX103101	HTM1-183F	599432 MA	AGENCOURT	

ALIGNMENTS

Query Match Best Local Similarity Matches 1049; Conser	gene	urce	TITLE I JOURNAL E COMMENT T	TITLE I JOURNAL S PUBMED S REFERENCE 2 AUTHORS C	REFERENCE AUTHORS	·
1 87.7%; Score 1048.4; DB 10; Length 1050; Similarity 99.9%; Pred. No. 2.1e-232; 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	/db_xref="taxon:9606" <1>1050 /gene="STEAP" /locus_tag="HCM1484"		Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M. Direct Submission Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA This sequence was made by sequencing genomic exons and ordering	Adams,M.D. and Cargili,M. Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios Science 302 (5652), 1960-1963 (2003) 14671302 2 (bases 1 to 1050) Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Mominidae; Homo. (bases 1 to 1050) (bases 1 to 1050) (Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Perriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,	AY403218 1050 bp DNA linear GSS 15-DEC-2003 Homo sapiens STEAP gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence. AY403218 AY403218.1 GI:39759201 GSS. Homo sapiens (human)

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Matches 934; Conserv
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2 (lark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Todd,M.A., Tanenbaum,C., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.
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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
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Mammalia, Eutheria, Euarchontoglires, Primates, Cata
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Science 302 (5652), 1960-1963 (2003)
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/db_xref="taxon:9598"
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Pred. No. 2.7e-205;
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EST.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Kristi A. Egland, Ira Pastan
cDNA Library Preparation: Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                 Hominidae; Homo.

1 (bases 1 to 884)

NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, |
Unpublished (1999)
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Mammalia; Eutheria; Euarchontoglires; Primates; Cata
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                                                                     GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC
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/note="Vector: pCMV-SPORT6; Site 1: EcoRV; Site 2: Not I;
/note="Vector: pCMV-SPORT6; Site 1: EcoRV; Site 2: Not I;
Subtracted with brain, liver, lung, kidney and muscle.
Directionally cloned. Priming method: oligo-dT. Average insert size: 1800 bp. Library amplification: 26,000 fold.
Kristi A. Egland, James J. Vincent, Robert Strausberg,
Bungkook Lee & Ira Pastan: Discovery of new breast
cancer genes encoding membrane and secreted proteins.
Manuscript submitted."
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hTERT-HME1, LNCap"
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/mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HTC; CAP trap
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Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H. Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okdo, T., Owa, C., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y.,
                                                                                                                                                                                                                                                                                         Group Phase I & II Team.
Analysis of the mouse transcriptome of 60,770 full-length cDNAs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
                                                                                                                                                                                                                                        Nature 420, 563-573
6 (bases 1 to 1211)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The RIKEN Genome Exploration Research Group Phase II Team and FANTOM Consortium.
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AK010437.1 GI:12845880
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1211 bp mRNA linear HTC 03-APR-2004
Mus musculus ES cells cDNA, RIKEN full-length enriched library,
clone:2410007B19 product:six transmembrane epithelial antigen of
                                                                                                                                                                                                                                                                                                                                                                      The FANTOM Consortium and the RIKEN Genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute c physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yoko Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URLihttp://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Suzuki,H., Tagami,M., Tagawa,A., Takahashi,
Tejima,Y., Toya,T., Yamamura,T., Yasunishi,
Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     details
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                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                             AGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCCATGCTAAAA
                                                                                                                                                                GTCATGGAGATCAGTGACGATGTTACAAACCCAGAACAACTTTGGAAAAATGAAGCCAAAG
                                                                                                                                                                                                                                                                GCGCCTCGCCGTCGGGTCCCACGGAGAAGCCGGTGGCTGAAGCCGTACTATTTTATAGCA
             AGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCA
                                                             GGAAACCTGGAAGATGACAGTTACTCGACTAAGGACTCGGGAGAGACGAGCATGCTGAAA
                                                                                                                                                                                           TTAATGGAAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTTGGAAAATGAAGCCTAGG
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EQYFYKIPILVINKLLPMVAITLLALYYLPGELAAVVQLRUGTKYKKEPDPWLDRWMLE
EQYFKIPILVINKLVINVAITLALYYLPGELAAVVQLVQQNKEDAWVEHDVWRMEI
KKQFGLLSFFFAVLHAVYSLSYPMRRSYRYKLLNWAYKQVQQNKEDAWVEHDVWRMEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="putative" 1211
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WVDVSQFVWYMPPTFMIAVFLPTLVLICKIALCLPCLRKKILKIRCGWEDVSKINRTE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /strain="C57BL/6J"
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/db_xxef="FANTOM_D000"
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81.0%;
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Pred. No.
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4e-176;
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Yasunishi, A.,
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Yoshida, K.,
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BLASTN, 100%,

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Mus musculus
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                                                                                                                                                                                              TAGAACTACTGTTTGCACATATTTGCTTGTTAT----TGATGTCCTATCATAAGCATTTC
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1 (bases 1 to 1050)

1 (bases 1 to 1050)

1 (clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
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AY403220.1
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This sequence was made by sequencing them based on alignment.
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Submitted (16-NOV-2003) Celera
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Science 302 (5652), 1960-1963 (2003)
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                                           CTGCCAGGTGTGATAGCAGCAATTGTCCCAACTTCATAATGGAACCAAGTATAAGAAGTTT
                                                                                      GACACGGGAGAGACCAGCATGCTAAAAAAGACCTGTGCTTTTTGCATTTGCACCAAACAGCC
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                  TIGCCAGGAGAGTTAGCGGCAGTTGTACAGCTTCGCAATGGAACCAAGTACAAGAAGTTC
                                                                                                                                                           CTGAGGGAAATCATCTACCCGTTAGTAACTTCCCGTGAACAATATTTTTATAAAATTCCA
                                                                                                                                                                                   CTGAGGGAAGTAATTCACCCTTTAGCAACTTCCCATCAACAATATTTTTATAAAAATTCCA
                                                                                                                                                                                                                                TGGCGCTTGCCAGTGAAAGTCGCTGCCATCATATCATCCCTGACTTTCCTGTACACACTT
                                                                                                                                                                                                                                                     TGGCACTTGCCAATTAAAATAGCTGCTATTATAGCATCTCTGACTTTTCTTTTACACTCTT
                                                                                                                                                                                                                                                                                                       CACGTCGATGCCTTTGACTGCCCCCTCCGAGCTTCAGCACACGCAGGAATTCTTTCCAAAC
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llarity 83.0%;
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/db_xref="taxon:10090"
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/locus_tag="HCM1484"
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0; Mismatches 178;
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TITLE
                                            source
                                                                                                              Hominidae; Homo.

18 (bases 1 to 720)

18 (NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

18 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

18 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

19 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

19 Tumor Gene Index

10 Unpublished (1997)

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13 Email: cgapbs-r@mail.nih.gov

14 Contact: Robert Strausberg, University of Iowa cDNA Library preparation: Dr. M. Bento Soares, University of Iowa cDNA Sequencing by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa clone Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, bento-soares@uiowa.edu
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720 bp mRNA linear EST 08-NOV UI-H-ED1-axr-o-23-0-UI.81 NCI_CGAP_ED1 Homo sapiens cDNA clone UI-H-ED1-axr-o-23-0-UI 3', mRNA sequence.
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CA446381.1 GI:24810801
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                                                     primer: M13 FORWARD
/organism="Homo sapiens"
/mol_type="mRNA"
                                                                 Location/Qualifiers
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Query Match
Best Local Similarity
                                                                                                                                                     476
  660
                                             / LINE TECHNOLOGIES) "
// Clone libe "NOI CGAP EDI"
// Clone libe "NOI CGAP EDI"
// Note = "Organ: Left Pubic Bone; Vector: pT7T3-Pac
// Note = "Organ: Left Pubic Bone; Vector: pT7T3-Pac
(Pharmacia) with a modified polylinker; Site 1: EcoR I;
Site 2: Not I; NCI CGAP EDI is a normalized GDNA library
containing the following tissue(s): Chondrosarcoma cell
line CS5. The library was constructed according to
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. First strand cDNA synthesis was primed with an
oligo-dT primer containing a Not I site. Double stranded
CDNA was ligated to an EcoR I adaptor, digested with Not
I, and cloned directionally into pT7T3-Pac vector. The
oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT).18 tail. The
sequence tag for this library is GCTCAAGGCT.
TAG TISSUE-chondrosarcoma
TAG_TIB=UI-H-ED1
TAG_SEQ=CGTCAAGGCT"
                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="Chondrosarcoma"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:9606"
/clone="UI-H-ED1-axr-o-23-0-UI"
                                                                                                                                                                                                                             60.1%;
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                                                                                                                                                                                                                                Score 718.4; DB Pred. No. 8e-156;
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                                                                                                                                                                                                                                                        DB 6;
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLCM1549 row: b column: 05
High quality sequence stop: 704.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: ggapbs-r@mail.nih.gov
Tissue Procurement: CLONETECH Laboratories, Inc.
CDNA Library Preparation: CLONETECH Laboratories, I
CDNA Library Arrayed by: The I.M.A.G.E. Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
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National Institutes of Health, Mammalian Gene Collection
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1 (bases 1 to 881)
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602582917F1 NIH_MGC_76 Homo sapiens cDNA clone IMAGE:4710436 5',
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//clone=11b="NIH_MGC_76"
/clone=11b="NIH_MGC_76"
/clone=11b="NIH_MGC_76"
/clone=11b="NIH_MGC_76"
/note="Organ: liver; vector: pDNR-LIB (Clontech); Site_1: fil (ggccgcctcggcc); Site_2: Sfil (ggccattatggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGGCCGACATG-GT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.85 kb (range 1.0-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."
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/mol_type="mRNA"
/db_xref="taxon:9606"
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92.0%;
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Pred. No. 7.2e-150;
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REFERENCE AUTHORS TITLE SOURCE ORGANISM ACCESSION VERSION COMMENT KEYWORDS Email: cgapbs r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLCM1713 row: h column: 21 Hominidae; Homo.

1 (bases 1 to 961)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian
Unpublished (1999)

Contact: Robert Strausberg, Ph.D. Plate: LLCM1713 row: h column: High quality sequence stop: 750. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homo sapiens BG762026.1 mRNA sequence. BG762026 GI:14072679

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DEFINITION

cDNA clone IMAGE:4858820 linear

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                                    AGGTCCAACAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTTGGAGAAT--GGAGAT
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AGGTCCAACAAATAAAGAAGATGCCTGGATTGAGCATGATGTTCGGAGAATGCGCCACT
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/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_49"
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/clone_lib="N
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Unpublished (2002)
Contact: DNA Core Facility (Bovine
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Prather, R.S., Antoniou, E., Garverick, H.A.,
Roberts, R.M., Smith, M.F. and Youngquist, R.S.
USDA Grant NRI-2002-03476: Bovine ESTs: Foo
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Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
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Fax: (573)884-5552
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Library construction (Standard Protocol): All procedures have been described in detail elsewhere (Soares et al., 1994; Bonaldo et al., 1996; Jiang et al., 2001). Total cellular RNA from each sample was isolated by using STAT-60 reagent (Tel-Test, Friendswood, TX) and the poly(A)+ RNA was obtained by two rounds of purification with the Oligotex mRNA isolation kit (Qiagen) according the manufacturer's instructions. The libraries were constructed essentially as described by the manufacturer's
                                                                                                                                                                                                                                                                                                                                                                                                          (http://www.circlearanch.com/home.html). These heifers, while not registered have known Angus pedigrees going back at least 4 generations. Samples collected: The samples consisted of the following: germinal vesicle-stage occytes; in vitro derived embryos (2-cell, morula) hastocyst and nuclear transfer blastocyst); in vivo blastocysts and conceptuses (days 8, 14, 16 and 18); corpora lutea (days 3, 5, 8, 14, 16, 18 and 35); ovarian follicles (days 0, non-recruited, recruited, early
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Vector: pSport1; Funding: The production of ESTs submitted in this project was funded by USDA Grant MRI-2002-03476 entitled 'Bovine ESTS: Focus on Female Reproduction' to RS Prather(Primary Investigator), E Antoniou, HA Garverick, JA Green, MC Lucy, RM Roberts, Smith and RS Youngquist. Genetic Source: Heifers for the project were purchased from Circle A Ranch, Iberia, MO
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                                                                                                                                                                                                                                                                          selected and preovulatory); oviduct (days 0, 3 and 5); endometrium (days 5, 8, 14, 16, 18 and 35); and placenta/embryo from day 35 conceptuses. Expanded descriptions of how the tissues were collected can be found at the following URL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
/db_xref="taxon:9913"
/dev_stage="Conceptus-Corpus Luteum(mixed)"
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                                                                                                                                         AGGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTA 179
                                                                                                                                                                                                AATTAAATGGAGAGAGACAAGACATCACAAAACCAAGAAGAACTTTGGAAAATGAAGCCT
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AGGAGAAATCTAGAAGAAGATGATTATTTGAATAAAGACTCAGAAGAGATCGGCATGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (mega-library) for more extensive sequencing.
Bioinformatics work was performed by GK Springer's bioinformatics group in Computer Science at the University of Missouri-Columbia. Clone Requests: Requests for clones should be made to the Director of the University of Missouri DNA Core facility at: bovine@rnet.missouri.edu. Citations: Bonaldo MF, Lennon G, Soares MB, Normalization and Subtraction: Two approaches to facilitate gene discovery. Genome Res, 1996; 6:791-806. Jiang H, Bivens NJ, Ries JE, Whitworth KM, Green JA, Forrester LJ, Springer GK, Diddion BA, Mathialagan N, Prather RS, Lucy MC (2001) Constructing cDNA libraries with fewer clones that contain long poly(dA) tails. Bioteem MB, MF and MG, P Jelene, L Su, L Lawcon, A Efstrantiadis. 1994. Construction and characterization of a normalized cDNA library. Proc Natl Acad Sci,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             library were analyzed by restriction digestion to determine average insert size (96 clones) and by sequencing (-4 96-well plates) to confirm library quality [e.g. the presence of short polyA+ tails, genomic DNA contamination (must be <1%), ribosomal RNA clones (must be <1%), etc.] and to provide a sequence database representing the predominant clones in each library. The clones were sequenced at the University of Missouri-Columbia DNA Core Facility. After production of the libraries, equal numbers of recombinants from each library were pooled to produce a single mixed library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          columns (Invitrogen-Life technologies). The cDNAs derived from each developmental stage of a particular tissue were mixed on an equimolar basis and ligated directionally into the NotI and Sall sites of the pCNV-SPORT6 vector (Invitrogen). After ligation of the inserts, the plasmids were electroporated into DH10B bacteria. Preliminary Library Characterization: Randomly chosen clones from each library Characterization: Randomly chosen clones from each
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the oligonucleotide used to prime first-strand synthesis. Second strand synthesis was performed with T4 DNA polymerase in the presence of DNA ligase and RNase H. After second strand synthesis, the double-stranded cDNAs were ligated to SalI adapters (Invitrogen-Life Technologies) and digested with NoII. The cDNAs were size selected by passage through cDNA size fractionation
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TAG_SEQ=Not found"
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found through the I.M.A.G.E. Consortium/LLNL http://image.llnl.gov plate: LLAM9674 row: p column: 03 High quality sequence stop: 701. Location/Qualifiers Email: cgapbs-r@mail.nih.gov Tissue Procurement: DCTD/DTP/Gazdar Unpublished (1999)
Contact: Robert Strausberg, Ph.D. NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Hominidae, Homo.

1 (bases 1 to 7 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homo sapiens Homo sapiens (human) BE875216.1 CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be Gene Collection (MGC)

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                    DN997716

697 bp mRNA linear EST 17-MAY-2005
TC115356 Human breast cancer tissue, large insert, pCMV expression
library Homo sapiens cDNA clone TC115356 5' similar to Homo sapiens
six transmembrane epithelial antigen of the prostate 1 (STEAP1),
mRNA sequence
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/tissue_types"large_cell_carcinoma, undifferentiated"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 69"
/clone_start; RGC 69"
/clone_Torgan: lung; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
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RS Birkett, C., Cho, J., Gau, Y., Hamer, R., Kelly, S., Kovacs, K., Liu, Liu, X., Porter, J., Sachs, A., Shu, Y., Sun, Z., Wong, J., Wu, M., Zhang, X., Jay, G. and He, W.

High-throughput cloning of full-length human cDNAs directly frocent in the continuous continu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DN997716
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Technologies Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This EST submission is part of an on-going human full-length cloning project at OriGene Technologies, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   http://www.origene.com
Seq primer: pCMV6 5prime forward
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                     CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG
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(note="Organ: Mammary gland (cancer tissue); Vector:

(note="Organ: Mammary gland (cancer tissue); Vector:

pCMV6-XL5; Site 1: EcoR1; Site 2: Xhol/Sall compatibl

ligatio; Oligo-dT primed reverse transcription optimi

for large and GC rich mRNA transcripts, cDNA size

selection, optimized ligation for large inserts into

mammalian expression vector, random clones selected f

end sequence verification of full-length genes"
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="TC115356"
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/clone_lib="Human breast cancer tissue,
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                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: NCI
cDNA Library Preparation: Michael Brownstein Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNI
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information c
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGENCOURT 10016846 NIH MGC_142 Homo sapiens IMAGE:6496341 5', mRNA sequence.
                                                                                                                                                                                                                        Plate: LLCM2675 row: j column:
High quality sequence stop: 604.
                                                                                                                                                                                                                                                                                                                                                                                                    NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1999)
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1 (bases 1 to 773)
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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/tissue_type="mixed (pool of 40 RNAs)"
/lab host="PH10B (T1-phage-resistant)"
/clome libe="NIH MGC_142"
/note="vector: pDNR-LIB; Site 1: SfiI (ggccattatggcc);
/note="vector: pDNR-LIB; Site 1: SfiI (ggccattatggcc);
Site_2: SfiI (ggccgcctcggcc); Double-stranded cDNA was prepared from a pool of 40 cell line polyA+ RNAs (bladder - 2*, blood - 33.4*, brain - 5.6*, breast - 12.5*, colon - 4*, connective tissue - 1.4*, eye - 1*, intestine - 2.6*, kidney - 2.2*, liver - 5.7*, lung - 10.8*, NK-cell - 5.2*,
                                                                                                                                  /mol_type="mRNA"
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/clone="IMAGE:6496341"
                                                                                                                                                                              organism="Homo sapiens'
                                                                                                                                                                                                          ocation/Qualifiers
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Similarity
  GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA
                            GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA
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                                                                                         AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAAATGAAGCCTA
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                                                                                                                                                                                                                                                                                                                                                                                ovary - 4%, pharynx - 2.5%, prostate - 4.3%, salivary gland - 1.3%, and skin - 2.3%). 5' and 3' adaptors were used in cloning as follows:
5'-AAGCAGTGGTATCAACGCAGAGTGGCCATTACGGCCGG-3' and 5'-ATTCTAGAGGCCGAGCGGCGAGAGTGGCCACATG-dT(30) NN-3'. Full-length enriched library was constructed using the Clontech Creator SMART kit and size-selected to contain the >0.5 size fraction (other fractions present in NH MGC 141). Library created in the laboratory of M. Brownstein (NIMH NIH). Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                           55.0%;
99.1%;
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KEYWORDS
CX757709 742 bp m
AGENCOURT 41384224 NIH MGC 278 Homo
IMAGE:7772991 3', mRNA sequence.
CX757709
CX757709.1 GI:58054365
EST.
                                                              sapiens cDNA clone
                                                                             24-JAN-2005
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679 600 619 540 480

499 420 439 360 379 300 319 240

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REFERENCE
AUTHORS
TITLE
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                                                                                                                                                                             118 ANTTAATGGAAAGCAGAAAAGACGTCACAAACCAAGAAGAAATTTGGAAAATGAAGCCTA
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National Institutes of Health, Mammalian
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Betheeda, MD 20892
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Tissue Procurement: Meri Firpo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDNA Library Preparation: Express Genomics CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                     GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCCAGCATGCTAA 180
                                                                                                                                                                                                                                                                                                            CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG
                                                                                                                                                                                                                  AATTAATGGAAAGCAGAAAAGACATCACAAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120
AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT
                                                                                                                                                                                                                                                                               CTGAGACTCACGGTCAAGCTACGGCGAGGAGTGGGTGGCTGAAGCCATACTATTTTATAG
                                                                       GGAGAAATTTAGAAGACAACGATTATTTGCATAAGGACACGGGAGAGAGCCAGCATGCTAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                quality sequence start: 6 quality sequence stop: 726. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue types pluripotent cell line derived from
/tissue types pluripotent cell mass"
/lab host="DH10B TonA"
/clone lib="NIH MGC 278"
/clone lib="NIH Registry betained from pluripotent cell
line derived from blastocyst inner cell mass (cell line
HSF-1.14, NIH Registry designation UC01. Positive for OCT4
expression by rtPCR, positive for SSEA-3, SSEA-4,
TTa-1-81, TTa-1-60 by immunofluorescence. Negative for
SSEA-1 by immunofluorescence. Passage 35. This line is a
subclone of the parental line; the parental line was
subcloned to remove aneuploid cells). cDNA was primed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5'-pGACTAGTTCTAGATCGCGAGCGGCCCC(T) 25-3' and cloned into the EcoRV/NotI sites of pExpress-1. Size-selection >1.25 kb resulted in an average insert size of 1.9 kb. This primary library is non-normalized (normalized primary library is NIH MGC 279) and was constructed by Express Genomics (Frederick, MD). Note: this is a Mammalian Gene collection library."
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/db_xref="taxon:9606"
/clone="IMAGE:7772991"
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97.4%;
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Pred. No. 2.2e-141;
0; Mismatches 18;
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RESULT 14
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AUTHORS
TITLE
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                                                                                                                                                                                                                                        Email: Ggapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Sh.
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can l
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BI552907 783 bp mRNA linear EST 05-Si 603197827F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:5277295
                                                                                                                                                                                                                                                                                                                                                                                                                                   Hominidae; Homo.

1 (bases 1 to 783)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian

Unpublished (1999)
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                Plate: LLAM11700 row: e column:
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                                                                                                                                                                                     quality sequence stop: 769.
Location/Qualifiers
                                                 /mol_type="mRNA"
/db xref="taxon:9606"
/clone="IMAGE:5277295"
/tissue_type="hippocampus"
/lab host="DH10B"
/clone lib="NIH MGC_95"
/note="Organ: brain; Vector: pBluescriptR (modified
/note="Organ: brain; Vector: pBluescriptR (modified
pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI
                                                                                                                                               /organism="Homo sapiens"
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RESULT 15
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                                                     CX753134 825 bp m
AGENCOURT 40991781 NIH MGC 281 Homo
IMAGE:7780881 3', mRNA sequence.
CX753134
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sapiens
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Pred. No. 4.2e-141;
0; Mismatches 5;
                                                                                  sapiens cDNA clone
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Tissue Procurement: Meri Firpo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hominidae; Homo.

1 (bases 1 to 825)

NIH-MCC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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  CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG
                                                                                       CAGAACTTCAGCACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG
                                                                                                                                                                 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT
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                                                                                                                                     AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT
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                                          CAGAACTTCAGCACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /Clone lib="NIH MGC 281"
//Clone lib="NIH MGC 281"
//Clone | Togan: Blastcoyst; Vector: pExpress-1; Site 1:
ECORV; Site 2: Not1; RNA obtained from pluripotent cell
line derived from blastcoyst inner cell mass (cell line
HSF-6, NIH Registry designation UCO6. Positive for OCT4
expression by rtPCR, positive for SSBA-4,
Tra-1-81, Tra-1-60 by immunofluorescence. Negative for
SSEA-1 by immunofluorescence Passage 62. cDNA was primed
using oligo-dT primer:
5'-pGACTAGTCTGAGTCGCGAGCGCCCCC(T)25-3' and cloned into
the ECORV/NotI sites of pExpress-1. Size-selection >1.25
kb resulted in an average insert size of 2.0 kb. This
primary library is normalized (non-normalized primary
library is NIH MGC 280) and was constructed by Express
Genomics (Prederick, MD). Note: this is a Mammalian Gene
Collection library."
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blastocyst inner cell mass"
/lab_host="DH108 TonA"
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:7780881"
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TCCAACTTCATAATGAACCAAGTATAAGAAGTTTCCACACTTGGTTGG
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Search completed: December 5, 2005, 03:12:12 Job time: 5464.54 secs

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SUMMARIES

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Xu J, Dillon DC, Mitcham Kalos MD, Fanger GR, Day Wang A, Meagher MJ;

Ή̈́,

Harlocker SL, Jiang Y, Reed SG; Retter MW, Stolk JA, Skeiky YAW;

(CORI-) CORIXA CORP.

WPI; 2001-425873/45.

The present invention describes polynucleotide sequences (I) which encode prostate-specific proteins (II). (I) and (II) have cytostatic activity, and can be used in vaccine production and gene therapy. (I), (II), antibodies to (II), fusion proteins comprising (II), and isolated T cells prepared using (I) or (II) are used treat cancer in a patient. (I) and

Claim 1; Page 510; 543pp; English.

vaccines

New polynucleotide encoding a prostate-specific protein, monitoring and treating prostate cancer in a patient and

for diagnosing, for use in

45	44	43	42	41	40	39	38	37	36	ა 5	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20
•	825.6			825.6	•	825.6	827.2	1042.4	1044	1048	1048	1166	1174.4	1177	1177	1178	1180.4	1181.8	1182	1190	1193	1193	1193	1195	1195
69.1	69.1	69.1	69.1	69.1		69.1	69.2	87.2	87.4	87.7	87.7	97.6	98.3	98.5	98.5	98.6	98.8	98.9	98.9	99.6	99.8	99.8	99.8	100.0	100.0
3627	3627	3627	3627	3627	3627	3627	3627	1369	1369	1365	1365	1354	1229	1201	1177	1277	1198	1193	1198	1294	1193	1193	1193	1330	1330
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ACD02612	ACD02598	ACD02606	ACD02605	ACD02613	AAD07071	AAZ49396	ACD02601	ACD02631	ACD02632	ACD02630	ACD02599	ADQ22300	AAK52962	ADX33625	ADV73174	ADL46020	ACD02629	ACD02597	ACD02628	AAK51978	ADY92698	AAD07067	AAZ49395	ADY19959	ADY15575
Acd02612 cDNA enco	Acd02598 cDNA enco	Acd02606 cDNA enco	Acd02605 cDNA enco	Acd02613 cDNA enco	Aad07071 Human six	Aaz49396 Human STR	Acd02601 cDNA enco	Acd02631 STEAP-1 v	Acd02632 STEAP-1 v	Acd02630 STEAP-1 v	Acd02599 cDNA enco	Adq22300 Human sof	Aak52962 Human pol	Adx33625 Plant ful	Adv73174 Human col	Adl46020 Human ova	Acd02629 STEAP-1 v	Acd02597 cDNA enco	STEAP	Aak51978 Human pol	Ady92698 Human STE	Aad07067 Human six	Aaz49395 Human STR	Ady19959 DNA encod	Ady15575 DNA encod

ALIGNMENTS

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14-JAN-2000; 2000US-00483672
                                                                                                                              16-JAN-2001; 2001WO-US001574.
                                                                                                                                                     WO200151633-A2.
                                                                                                                                                                Homo sapiens.
                                                                                                                                                                            Human; prostate cancer; prostate-specific; diagnosis; vaccine; cytostatic; gene therapy; metastasis; ss.
                                                                                                                                                                                              P789P full length cDNA sequence.
                                                                                                                                                                                                          04-OCT-2001
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                         CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA
                                                                            ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC
                                                                                         ATGTGTCTCTGGGAATTGTGGGAATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC
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09-MAY-2000;
12-MAY-2000;
13-JUN-2000;
27-JUN-2000;
09-AUG-2000;
29-AUG-2000;
06-SEP-2000;
02-CCT-2000;
10-CCT-2000;
10-NOV-2000;
                                                                                                                     Fanger
Li SX,
 The invention relates to isolated prostate-specific polynucleotides, polypeptides, fusion proteins of the polypeptides, antibodies raised against the polypeptides (or antigenic epitopes derived from them) as
                                        Claim
                                                                                        WPI; 2001-639232/73.
P-PSDB; AAU69927.
                                                                                                                                                                                                                                                                                                                                                                              Human; prostate
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                                                                                                                                                           (CORI-)
                                                          human prostate-specific polypeptides and polynucleotides useful diagnosis and treatment of cancer, especially prostate cancer.
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                                                                                                                   Dillon DC, Mitcham JL, Harlocker SL, Jiang GR, Retter MW, Stolk JA, Day CH, Vedvick Wang A, Skeiky YAW, Hepler WT, Henderson I
                                                                                                                                                           CORIXA CORP.
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2000US-00593793.

2000US-00605783.

2000US-00636215.

2000US-00651236.

2000US-00657279.

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                                        English
                                                                                                                                                                                                                                                                                                                                                                               cytostatic;
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Carter D;
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Best Local Sim
Matches 1195;
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                                                                                                                                                                                                                                  GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC
                                                                                                                                                                                                                                                                                             CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAGTCTTGC
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TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG
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Pred. No. 4.4e-276;
Mismatches 0;
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                                                                                                                                                                                     (CART/
                                                                                                                                                                                                                                                  (FANG,
(RETT,
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(SKEI/
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HURAL J.

MCNEILL P D.

HOUGHTON R L.

Y DE BASSOLS

FOY T M.
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HEPLER W T.
HENDERSON R A.
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RETTER M W.
STOLK J A.
DAY C H.
VEDVICK T S.
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DILLON D C
MITCHAM J :
HARLOCKER :
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KALOS M D.
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Matches 1195;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Li SX, Wang A, Skeiky YAW, Hepler WT, Hendersen RA, Mcneill PD, Houghton RL, Y De BassolsCV, Foy TM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Prostate specific protein and its encoding treatment and diagnosis of prostate cancer
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                    CAATGGTTTCCATCACTCTCTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG
                                                                                                                                                                                                         CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC
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                                                             CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC
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25-FEB-1998
14-JUL-1998
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15-JAN-1999
09-APR-1999
13-JUL-1999
13-JUL-1999;
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herapy; gene; ss.
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29-AUG-2000
06-SEP-2000
06-SEP-2000
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10-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                   The present invention provides prostate-specific coding sequences and their encoded proteins. These can be used in the diagnosis and treatme of cancers, particularly prostate cancer. The present sequence is a cl described in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New prostate-specific polynucleotides for diseases, in particular prostate cancer, a progression of cancer.
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Fanger GR, Retter MW,
Li SX, Wang A, Skeik,
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) DILLON D C.
) MITCHAM J L.
) HARLOCKER S L.
JIANG Y D.
KALOS M D.
PANGER G R.
RETTER M W.
STOLK J A.
DAY C H.
VEDVICK T S.
CARTER D.
LI S X.
WANG A.
SKEIKY Y A W.
HEPLER W T.
HEPLER W T.
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CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG
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                                                           AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT
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2000US-00636215.

2000US-00637279.

2000US-00679426.

2000US-00685166.
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er MW, Stolk JA,
Skeiky YAW, Hep
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Pred. No. 4.4e-276;
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JA, Day CH, Vedvick 
Hepler WT, Henderson I
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BSULT 5 BK92128 D ABK92128 standard; DNA; 1195 BP. X C ABK92128;

T 15-AUG-2002 (first entry) X

)E Prostate cancer-associated DNA sequence #14.

Prostate cancer; prostate tumour tissue; human; mammal; cytostatic;

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                                                                                                                                                                                                                                                 The present invention relates to methods of detecting a prostate cancer-
cc associated transcript in a cell from a patient. The method comprises
cc contacting a biological sample from the patient with prostate cancer-
cc associated polynuclectides (designated PC genes) that selectively
cc hybridise to a sequence that is at least 80% identical to them. The
cc prostate cancer-associated polynuclectide sequences are differentially
cc expressed in prostate tumour tissue or in prostate cancer and are derived
cc (e.g. mice, sheep and dogs). The methods of the invention are useful for
cc diagnosing and treating prostate cancer in mammals. The prostate cancer,
cc associated genes are useful for diagnosing or treating prostate cancer,
cc as well as for identifying medulators of prostate cancer or agents that
cc inhibit prostate cancer. The nucleix acid sequences are particularly
cc useful in gene therapy, as a vaccine or in antisense applications.
cc ABK92115-ABK92263 represent prostate cancer-associated polynucleotide
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Best Local Sim
Matches 1195;
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08-DEC-2000;

08-DEC-2000;

24-JAN-2001;

16-MAR-2001;

16-MAR-2001;

06-APR-2001;
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DB; ABG61813.
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            AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT
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2000US-00733742.
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ACC95695 standard; cDNA; 1195

ACC95695;

(first entry)

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Query Match
Best Local S
Matches 1195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New prostate-specific proteins and genes, useful in gene therapy, particularly for stimulating an immune response in a patient, or treating prostate cancer in a patient, as well as for diagnosing prostate cancer
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Kalos MD, Fanger RR, Retter MW, Stock JA, Day CH, Vedvick TS;
Carter D, Li SX, Wang A, Skeiky YAW, Hepler WT, Hural J;
Mcneill PD, Houghton RL, Vinals Y De BassolsC, Foy TM, Watanabe
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29-JUN-2001; 2001US-00895814.
10-DEC-2001; 2001US-00012896.
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22-AUG-2001; 2001US-0314356P.
25-SEP-2001; 2001US-0325020P.
12-DEC-2001; 2001US-0341746P.
05-MAR-2002; 2002US-0362158P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1195 BP; 382 A; 221 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to newly discovered cancer markers associated with the cancerous state of prostate cells. Also disclosed is a method of assessing whether a patient is afflicted with prostate cancer. The method of the invention involves assessing whether a patient is afflicted with
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Human, ss, prostate specific cDNA; cytostatic; immunostimulant; gene therapy; cell therapy; vaccine; T-cell epitope; class I major histocompatibility complex allele; MHC; prostate
                                                                                                                                                                      Human prostate specific full length cDNA P789P
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12-NOV-2002; 2002US-00294025

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CC alleles. ADBI3563 is a polypeptide encoded by a human prostate specific CC cDNA, one of 648 disclosed as new. Also included are nucleic acids cencoding the proteins and peptides, expression vectors, a host cell cransformed with the vector, an isolated antibody (or antigen binding fragment) that specifically binds to the protein or peptide, detecting CC the presence of a cancer in a patient (comprising contacting a patient CC sample with a binding agent that binds to the peptides or a polypeptide CC sample with a binding agent that binds to the peptide to a predetermined cut the agent and comparing the amount of polypeptide to a predetermined cut off value to determine the presence of cancer), a fusion protein CC comprising the peptides or proteins, stimulating or expanding T cells specific for a tumour protein, stimulating or expanding T cells specific for a tumour protein a composition comprising the peptides, conclete acids, antibodies or compounds, determining the peptides, concer in a patient and treating prostate cancer in a patient with the peptides or antigen presenting cells that express CC (the peptides so that the T cells proliferate, and administering the peptides (that hybridises to nucleic acide encoding them), is used to detect the concretin a patient. The peptides, nucleic acide encoding, or antigen-presenting cells expressing the nucleic acide encoding.
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14-JAN-2000)
27-MAR-2000
29-MAY-2000
112-MAY-2000
112-MAY-2000
112-MAY-2000
112-MAY-2000
109-AUG-2000
09-AUG-2000
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14-JUL-1998
23-SEP-1998
15-JAN-1999
09-APR-1999
13-JUL-1999
12-NOV-1999
18-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                         11-542 amino acids of ADB13563 comprising a sequence ADB14487. The peptides comprise a fragment ADB13563 of that contain naturally processed T-cell epitopes for 3 class I major histocompatibility complex (MHC) alleles. ADB13563 is a polypeptide encoded by a human -----
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2000US-00536857.
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2000US-00593793.
2000US-00605783.
2000US-00636215.
2000US-00657236.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             polypeptide for use in a vaccine for stimulating an immune for treating or diagnosis cancer, preferably prostate
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                                                                                        The present invention relates to a method of prognosticating metastasis in a breast cancer patient involves identifying differential modulation of each gene relative to the expression of the same genes in a normal population in combination of genes. The invention is useful for prognosticating breast cancer in a patient. The present sequence is huma STEAP (six transmembrane epithelial antigen of the prostate) DNA used to illustrate the method of the invention
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25-FEB-1998; 98US-00020956.
25-FEB-1998; 98US-0015453.
23-SEP-1998; 98US-00159812.
15-JAN-1999; 99US-00232149.
09-APR-1999; 99US-00232149.
15-JOUL-1999; 99US-00443686.
13-JUL-1999; 99US-00443686.
14-JAN-2000; 2000US-00536857.
27-MAR-2000; 2000US-00536857.
29-AMAY-2000; 2000US-00568100.
12-MAY-2000; 2000US-0059793.
27-JUN-2000; 2000US-0059793.
27-JUN-2000; 2000US-0059793.
27-JUN-2000; 2000US-00657236.
09-AUG-2000; 2000US-00657236.
09-AUG-2000; 2000US-00657236.
10-OCTT-2000; 2000US-00657236.
10-OCTT-2000; 2000US-00657236.
10-OCTT-2000; 2000US-0065729.
12-JAN-2001; 2001US-0079729.
12-JAN-2001; 2001US-00759143.
09-FEB-2001; 2001US-00759143.
29-JUN-2001; 2001US-00852911.
29-JUN-2001; 2001US-00852914.
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Carter D, Li SX, Wang
Mcneill PD, Houghton R
Meagher MJ, Deng T;
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         The invention relates to human prostate-specific polypeptides and the polynucleotides encoding them. The invention also relates to an isolated antibody or its antigen-binding fragment that specifically binds a polypeptide of the invention, a method of detecting cancer in a patient comprising contacting a biological sample of the patient with an agent that binds a prostate-specific polypeptide and comparing the amount of bound polypeptide compared to a predetermined cut-off value and a fusion protein comprising a prostate-specific polypeptide. The sequences of the invention are used to diagnose and treat cancer, particularly prostate cancer. This sequence represents cDNA encoding a human prostate-specific polypeptide of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html.
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hton RL,
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Retter MW, Stolk JA, Day Th, Vedvick TS;
ng A, Skeiky YAW, Hepler WT, Hural J;
RL, Vinals Y De BassolsC, Foy TM, Watanabo
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                                                                                    TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG
                                                                                                                               CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA
                                                                                                                                           CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA
                                                                                                                                                                                     ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC
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                                                                                                                                                                                                                                  AGGTCCAACAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT
TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA
                TTGTTGTTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA
                                                   ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTACAA
                                                                                                TIGITTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG
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Pred. No. 4
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RESULT 12
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ADN39812
AC ADN39
XX ADN39
XX TOTAL
ACT ADN39
XX Cance
XX Human
XW Fibro
KW Fibro
KW Getec
KW Wound
XX Vulne
OS Homo
XX WO200
PM WO200
XX 13-NC
XX 13-NC
PR 29-MJ
PR 10-JJ
PR
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13-FEB-2002;
20-FEB-2002;
29-MAR-2002;
04-APR-2002;
11-APR-2002;
05-JUN-2002;
16-JUL-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-NOV-2001;
21-NOV-2001;
29-NOV-2001;
03-DEC-2001;
04-DEC-2001;
08-JAN-2002;
10-JAN-2002;
                       Claim 8; SEQ ID
                                                                   Determining the presence or absence of a pathological cell in a patient, useful for diagnosing, prognosing or treating cancer, comprises detecting a nucleic acid in a biological sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  detection; diagnosis; prognosis; drug screening; druound healing; contraception; cytostatic; cardiant;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     inflammatory disease; autoimmune disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-JUN-2004
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Murray
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2001US-0332464P.
2001US-033439AP.
2001US-0335394P.
2002US-0347211P.
; 2002US-0347211P.
; 2002US-0355250P.
; 2002US-0356714P.
; 2002US-0356714P.
; 2002US-0359077P.
; 2002US-0368809P.
; 2002US-0370110P.
; 2002US-0370110P.
; 2002US-0372246P.
; 2002US-0397845P.
; 2002US-0397845P.
; 2002US-0397845P.
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                                                                                                                                                                                                                               Ginsburg WM,
R, Watson SR,
                       C184; 1385pp; English
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Wilson
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E, Zlotnik
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nt; immunomodulatory;
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Best Local
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                                  AGGTCCAACAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT
                                                                    GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC
                                                                                      GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC
                                                                                                                                       CAATGGTTT
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13-NOV-2001; 2001US-0350666P.
21-NOV-2001; 2001US-03343494P.
29-NOV-2001; 2001US-0333394P.
03-DEC-2001; 2001US-0335394P.
14-DEC-2001; 2001US-0340376P.
08-JAN-2002; 2002US-0347211P.
10-JAN-2002; 2002US-0347349P.
08-FEB-2002; 2002US-0355250P.
13-FEB-2002; 2002US-0355250P.
13-FEB-2002; 2002US-0359077P.
29-MAR-2002; 2002US-0358809P.
04-APR-2002; 2002US-035634P.
15-JUN-2002; 2002US-0386614P.
16-JUL-2002; 2002US-0396839P.
                                                                                                                                                                                                                                                                                                      detection; diagnosis; prognosis; drug screening; drug targeting; wound healing; contraception; cytostatic; cardiant; immunomodulatory; vulnerary; gene therapy; vaccine; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                          Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADN39395 standard;
                                                                                                                                                                                                        13-NOV-2002;
                                                                                                                                                                                                                                22-MAY-2003
                                                                                                                                                                                                                                                         WO2003042661-A2
                                                                                                                                                                                                                                                                                                                                              retinal neovascularistaion syndrome; scarring; uterine fibroid;
                                                                                                                                                                                                                                                                                                                                                                      Human; differential expression; cancer; fibrotic disorder; psoriasis; ischaemia;
                                                                                                                                                                                                                                                                                                                                                           Inflammatory disease; autoimmune disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    entry)
                                                                                                                                                                                                                                                                                                                                                                      angiogenic diso;
; heart disease;
                                                                                                                                                                                                                                                                                                                                                                                    disorder;
                                                                                                                                                                                                                                                                                                                                                                                                             ID NO:B79
                                                                                                                                                                                                                                                                                                                                                                       atherosclerosis;
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Best Local Similarity
Matches 1195; Conserv
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22-JUL-2002;
09-SEP-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1195 BP; 382 A; 221 C; 233 G; 359
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DB; ADN39396.
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Murray R,
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CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG
                                                                CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC
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                                                                                                                                       CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG
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; 2002US-0397845P.
; 2002US-0409450P.
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R, Watson
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¬SR,
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Pred. No. 4.4e-276;
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Wilson F
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E, Zlotnik
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          31-MAR-2003; 2003EP-00252027
                                                                                                                                                                  ADP88258
                                                                                                                                                                                     ADP88258 standard;
                                                                                                          Diagnostic marker; portfolio; diagnostic
                                                                                                                                                12-AUG-2004
                            01-OCT-2003
                                                                                                  relative expression;
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                                                                                portfolio; human;
                                                                                         marker; portfolio; diagnostic parameter; gene expression; expression; heuristic rule; molecular diagnostic; diagnosis cancer; breast; prostate; ovarian; colorectal; lung;
                                                                                                                                                (first
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                                                                                                                             STEAP,
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The invention relates to a method of selecting a portfolio of markers (C (e.g., genes) for use in a diagnostic application. The method involves: (a) defining diagnostic parameters; (b) establishing a relationship among the diagnostic parameters so that they are optimised; and (c) selecting the diagnostic parameters so that they are optimised; and (c) selecting the optimal group of markers (the portfolio) for the diagnostic c application. The diagnostic parameters can include a measure of the relation in the measurement of the degree of gene, a measure of the variation in the measurement of the degree of gene expression, and the relationship relative degree the diagnostic parameters can be a mean comparison that the relationship determines the relationship. The method further comprises the application of a heuristic rule. The invention also relates to a general-purpose computer programmed to identify a portfolio of markers, instructions for comprising genes selected according to the method. The method of the computer programmed to identify a portfolio of markers, instructions for determining gene succession. The method of the method of the compression of relevant cells as well as protein-based methods of the expression of relevant cells as well as protein-based methods of compensation of multiple genes (e.g., breast, prostate, ovarian, cc colorectal or lung cancer). By grouping these markers into portfolios, the most reliable results can be obtained with the smallest number of markers necessary to obtain such a result, which is particularly component sequence represents a human diagnostic marker gene that is a member of an optimised portfolio of 31 genes for screening for prostate, breast, colon, ovarian and lung cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Selecting a portfolio of markers useful in diagnostic applications comprises defining diagnostic parameters and establishing a relationship among the diagnostic parameters that identifies an optimized portfolio of markers.
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Query Match Best Local S Matches 1195 Sequence Local Sinhes 1195; Similarity 100.0%; Score 1195; DB 11; ilarity 100.0%; Pred. No. 4.4e-276; Conservative 0; Mismatches 0; BP; 382 A; 221 C; 233 G; 359 <u>;</u> 0 U; Indels Length 1195; 0 Other; 0

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21-AUG-2002;
23-SEP-2002;
15-OCT-2002;
15-NOV-2002;
02-JUL-2003;
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P-PSDB; ADL06542.
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ALIGNMENTS

REFERENCE AUTHORS TITLE RESULT 1
CQ776742
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Matches 1195; Conserva JOURNAL 61 _ Ь pulmonary disease Patent: EP 1394274-A 428 03-MAR-2004; Genox Research, Inc. (JP) Location/Qualifiers Sequence 428 from Patent CQ776742 CQ776742.1 GI:45380132 Ohtani, N., Sugita, Y., Yamaya, M., Kubo, H Methods of testing for bronchial asthma Eukaryota; Metazoa; Mammalia; Eutheria; Homo sapiens CQ776742 Hominidae; Homo. Homo sapiens (human) AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG Conservative /organism="Homo sapiens" /mol_type="unassigned DN /db_xref="taxon:9606" 100.0%; Score 1195; DB 6; 100.0%; Pred. No. 5.5e-238; tive 0; Mismatches 0; Chordata; Craniata; Vertebrata; Euteleo Euarchontoglires; Primates; Catarrhini; 1195 bp : EP1394274 DNA" Kubo, H., DNA ç Nagai,H. or chronic Length 1195; Indels linear and Izuhara, K. obstructive Euteleostomi; PAT 0 11-MAR-2004 Gaps 60 0

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Afar,D.E., Hubert,R.S.,
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S Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,

Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,

Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W.,

Vedvick,T.S., Carterson,R.A.

Compositions and Henderson,R.A.

Compositions and methods for the therapy and diagnosis of procancer

L Patent: US 6630305-A 878 07-OCT-2003;

Corixa Corporation; Seattle, WA;

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/organism="unknown"
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Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W.,
Hepler,W.T. and Henderson,R.A.
Compositions and methods for the therapy and diagnosis of p
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Corixa Corporation; Seattle, WA
Location/Qualifiers
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              AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTTGGAGAATGGAGATTT
                                                            GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC
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/mol_type="genomic
                                           ACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC
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Pred. No. 5.5e-238;
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Sequence
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Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y
Xu,J., Di, Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H
Kalos,M.D., Fanger,D., Li,S.X., Wang,A., Skeiky,Y.A.W.,
Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W.,
Hepler,W.T. and Henderson,R.A.
                                                                                                                                                                                                                                                                                                                                                                                                        Unclassified
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                                                                                                                                                                                                                                                                                            Patent: US 6800746-A 878 05-OCT-2004;
                                                                                                                                                                                                                                                                                                                         Compositions and methods for the therapy
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Afar,D.E., Hubert,R.S., Leong,K., Rai
Mitchell,S.C.
Peptides derived from STEAP1
Patent: US 6887975-A 1 03-MAY-2005;
Agensys, Inc., Santa Monica, CA
Agensys, Location/Qualifiers
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                                                                     GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC
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121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGCCCAGCATGCTAA 180	61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120	1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60	Watch 100.0%; Score 1195; DB 6; Length 1195; Local Similarity 100.0%; Pred. No. 5.5e-238; hes 1195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	/or /mo /db		AU,J., DILION,J.C., MICCHAM,J.L., HATIOCKEY,S.L., JIENG,X., Reed,S.G., KALOS,M.D., Panger,G.R., Day,C.H., Retter,M.W., Stolk,J.A., Skeiky,Y.A., Wang,A. and Meagher,M.J. Compositions and methods for the therapy and diagnosis of prostate cancer	ia; Eutheria; Euarchontoglires; Pdae; Homo.	Homo sapiens (human) Homo sapiens Eukarvota: Metazoa:	AX201105 1195 bp DNA linear PAT 29-AUG-2001 Sequence 735 from Patent WO0151633. AX201105 AX201105.1 GI:15390890		141 TCAAGTTTGTATTAATAAAATGATTATTCAAGGAAAAAAAA	081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATT 1140	021 AGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT 1080	961 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1020 	901 ATATAAACAATTIGTATGGTATACACCTCCAACTTITATGATAGCTGTTTTCCTTCCAA 960 	841 TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 900	781 CATCTGTGAGTGACTCTTTGACATGGAGAGAGTTTCACTATATTCAGAGCAAGCTAGGAA 840	
RESULT 8 AX267904	B 45	D &	S B &	gb Qy	dg Qy	ФУ	ρ γ	dp dy	Qy Db	da Vy	р <i>Қ</i>	g 8 4	\$ B &	D Dy	B &	S B 8	ov DB	g vg
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Compositions and methods for the therapy and diagnosis of prostat
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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/organism="Homo sapiens"
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Panel of nucleic acid sequences for cancer Patent: EP 1355150-A 35 22-OCT-2003; Ortho-Clinical Diagnostics, Inc. (US) Location/Qualifiers
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              GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC
                                                CAATGGTTTCCATCACTCTTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG
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/mol_type="unassigned DN/
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Ouery Match 100.0%; Score 1195; DB 6; Length 1195; Best Local Similarity 100.0%; Pred. No. 5.5e-238; Matches 1195; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Oy 1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGAGGCCATACTATTTATAG 60	Ortho-Clinical Diagnostics, Inc. (US) FEATURES Location/Qualifiers source 1. 1195 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"		RESULT 11 AX960014 AX960014 LOCUS AX960014 DEFINITION Sequence 35 from Patent EP1349104. ACCESSION AX960014 VERSION AX960014 VERSION AX960014 GI:40880240 KEYWORDS SOURCE Homo sapiens (human)		961 TIGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATACTAAAACTAAAACTAAAACTAAAACTAAAACTAAAACTAAAACTAAAACTAAAACTAAAACTAAAACTAAAACTAAAACTAAAACTAAAACTGAAAAATTAACAAAAATTAACAAAAATTAACAAAAACTGAAAAATTAACAAAAACTGAAAAATTAACAAAAACTGAAAAATTAACAAAAACTGAAAAATTAACAAAAATTAACAAAAATTAACAAAAATTAACAAAAATTAACAAAAATTAACAAAAATTAACAAAAATTAACAAAAATTAACAAAAATTAACAAAAATTAACAAAAATTAACAAAAATTAACAAAAATTAACAAAAATTAACAAAAATTAACAAAAATTAACAAC	841 TIGTTICCCTTCTACTGGGCACAATACACGCATTGATTTTTTGCCTGGAATAAGTGGATAG 901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCC	Oy 661 AGGTCCAACAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATTGTTTTTTTT
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1021 AGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT 1080	ATATAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCC		661 AGGTCCAACAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTTGAGAATGGAGATTGT 720	541 TAACAAGAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCA	421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480	301 CTATTATAGCATCTCTGACTTTTTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360	121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180 121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180 181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCATGCTGATGAATTTGACTGCCCTT 240

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Hubert, R.S., Vivanco, I., Chen, E., Rastegar, S., Leong, K.,
Mitchell, S.C., Madraswala, R., Zhou, Y., Kuo, J., Raitano, A.B.,
Jakobovits, A., Saffran, D.C. and Afar, D.E.
STEAP: a prostate specific cell-surface antigen highly expressed
human prostate tumors
Proc. Natl. Acad. Sci. U.S.A. 96 (25), 14523-14528 (1999)
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AF186249
AF186249.1 GI:6572947
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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YVSLGIVGLAILALLAVTSIPSVSDSLTWREFHYIQSKLGIVSLLLGTIHALIFAWNK
WIDLKQFVMYTPPTFMIAVFLPIVVLIFKSILFLPCLRKKILKIRHGWEDVTKINKTE
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CQ981397 1330 bp DNA linear PAT 25-JAN-2005 V Sequence 252 from Patent EP1498424. CQ981397 CQ981397.1 GI:58190687	.141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAA	081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTTATT	021 AGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATA	GATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTC	961 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1020 	A 96	41 TIGTTTCCCTTCTACTGGGCACAATACACGCATIGATITITUSCCTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	41 TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 90	781 CATCTGTGACTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 040	21 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 78	721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 780	racaaaataaagaagatgcctggattgagcatgatgtttggagaaatggag	601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660 	41 TAACAAGAAAGCAGTTTGGGGCTTCTCAGTTTTTTTGCTGTACTGCAGTCTATATA 6	aacaagaaagcagtttgggcttctcagtttcttttttttgctgtactgcat	481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGG	21 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 4	21 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 48	361 CAACTICCCATCAACAAIAIIIITATAAAAIICCAAICCISSICAICAACAAGTCTISS 120 120 120 120 120 120 120 120 120 120	01 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTAG 30	01 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTTAG 36	41 CAGAACTTCAGCACACACAGAGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG	41 CAGAA	181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240

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Mammalia; Eutheria; E
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                                                                                                                                                                                                                                         CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Pred. No. 5.4e-238;
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                diseases
                                                                                                                                                                                                                                                                                             Abbas, A., Clark, H., Ouyang, W., Williams, M.P., Compositions and methods for the treatment of
                                                                                                                                                                                                                                                         Genentech, Inc. (US)
                                                                                                                                                                                                                                                                    Patent: WO 2005016962-A 1381
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/mol_type="unassigned DN
/db_xref="taxon:9606"
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CS036259.1
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT
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                                                                     GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC
                                                                                    GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC
                                                                                                                            TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTTCTTTTTTGCTGATGCCATGCAATTTATA
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/mol_type="unassigned DN/
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CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA
ATGTGTCTCTGGGAATTGTGGGAATTGGCAATACTGGCTCTGTTGGCTGACATCTATTC
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Search completed: December 5, 2005, 00:23:41 Job time: 6322.97 secs

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1: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*

2: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*

3: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*

4: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*

5: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*

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7: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*

9: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*

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  US-10-750-185-59979
US-10-750-185-25365
US-10-750-185-26044
US-11-145-703-1
US-10-750-185-36894
US-10-750-185-32077
US-10-750-185-51935
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Sequence 5977, A
Sequence 25365, A
Sequence 39315, A
Sequence 30144, A
Sequence 1, Appli
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Sequence 57750, A
Sequence 51935, A
Sequence 46765, A
Sequence 51935, A
Sequence 51935, A
Sequence 51935, A
Sequence 27, Appl
Sequence 22, Appl
Sequence 163, App
Sequence 152, App
Sequence 152, App
Sequence 25062, A
Sequence 25063, App
Sequence 49060, A
Sequence 49060, App
Sequence 27479, App
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2.9	2.9	2.9	2.9	2.9	2.9	2.9	2.9	2.9	2.9	2.9	2.9	2.9	2.9	2.9	2.9	2.9	2.9	2.9	2.9	3.0
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Sequence Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
367, App 40313, A	63164, A	54610, A	50, Appl	47, Appl	49, Appl	57482, A	52014, A	5, Appli	5, Appli	30480, A	51951, A	40261, A	61634, A	547, App	49, Appl	42494, A	44612, A	46490, A	5, Appli	41075, A

ALIGNMENTS

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GENERAL INFORMATION:

APPLICANT: MMI GENOMICS, INC.

APPLICANT: DENISE, SUE K.

APPLICANT: ENERGY, RICHARD

APPLICANT: KERR, RICHARD

APPLICANT: ROSENFELD, David

APPLICANT: BATES, Stephen

APPLICANT: BATES, Stephen

APPLICANT: FANTIN, Dennis

TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS

FILE REFERENCE: MMI1100-2

CURRENT APPLICATION NUMBER: US/10/750,185

CURRENT APPLICATION NUMBER: US 60/437,482

PRIOR APPLICATION NUMBER: US 60/437,482

PRIOR FILLING DATE: 2002-12-31

NUMBER OF SEQ ID NOS: 64922

SOFTWARE: PATENTIN VETSION 3.1

EQ ID NO 59979
RESULT 2
US-10-750-185-25365
; Sequence 25365, Application US/10750185
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US-10-750-185-59979
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US-10-750-185-59979/c
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Publication No. US20050260603A1
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APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MM11100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
VIMBER OF SEQ ID NOS: 64922
SOFTWARE: Patentin version 3.1
SEQ ID NO 39315
LENGTH: 2464
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CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTMARE: PATENTIN VERSION 3.1
SEQ ID NO 25365
LENGTH: 1779
TYPE: DNA
OPCANISM: BOX: 10866886604013
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US-10-750-185-39315
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US-10-750-185-25365
                                                                                          Query Match
Best Local S
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APPLICANT: DENISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 39315, Application US/10750185
Publication No. US20050260603A1
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Best Local Similarity 54.1%;
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APPLICANT: MMI GENOMICS, INC.
APPLICANT: DENISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
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TITLE OF INVENTION: COMPOSITIONS FOR INFERRING
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96; Conserv
                                      GCAAGCTAGGAATTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGA
   AGAGAAAGGGAAAATTCTGGAATATAAAATGCCATTCTGCAGTATATCTGCAGTCTCAAT 1689
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HOLM, Tom
BATES, Stephen
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Pred. No. 2.7;
0; Mismatches 9
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                                                                                                                Length 2464;
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APPLICANT: MMI GENOMICS, INC.
APPLICANT: DANISE, Sue K.
APPLICANT: ERRR, Richard
APPLICANT: ROSENFELD, David
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: HOLM, Tom
APPLICANT: FANTIN, Dennis
ITITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMI1100-2
FILE REFERENCE: MMI1100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT APPLICATION NUMBER: 003-12-31
PRIOR APPLICATION NUMBER: 06/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: Patentin version 3.1
SEQ ID NO 26044
LENGTH: 2133
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US-10-750-185-26044
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RESULT 5
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Best Local Similarity
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ORGANISM: Bovine
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Pred. No. 3.2;
0; Mismatches 134; Indels
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US-11-145-703-1/c; Sequence 1, Application US/11145703; Publication No. US20050260667A1

GENERAL INFORMATION:
APPLICANT: Cohen, Daniel
APPLICANT: Blumenfeld, |
APPLICANT: Chumakov, II

Blumenfeld, Ma Chumakov, Ilya

Marta

Bougueleret, Lydie Bihain, Bernard

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SOFTWARE: Patent.pm
SEQ ID NO 1
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PRIOR FILING DATE: 2000-03-30
PRIOR APPLICATION NUMBER: 09/539,333
PRIOR FILING DATE: 2000-03-30
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PRIOR FILING DATE: 1999-03-30
PRIOR APPLICATION NUMBER: US 60/131,971
PRIOR FILING DATE: 1999-04-30
PRIOR FILING DATE: 1999-04-30
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CURRENT FILING DATE: 2000-03-30
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NAME/KEY: misc_feature
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TYPE: DNA
ORGANISM: Homo sapiens
                                                 FEATURE:
NAME/KEY: exon
LOCATION: 65505..65853
OTHER INFORMATION: exon
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LOCATION: 29967..30282
OTHER INFORMATION: exor
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LOCATION: 29388..29502
OTHER INFORMATION: exon
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LOCATION: 1108..1289
OTHER INFORMATION: ex
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OTHER INFORMATION: exon
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LOCATION: 14877..14920
OTHER INFORMATION: exor
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OTHER INFORMATION: 5'regulatory region g35018 gene
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AME/KEY: misc_feature
OCATION: 65854..67854
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TLE OF INVENTION: SCHIZOPHRENIA ASSOCIATED GENES, PROTEINS AND BIALLELIC MARKE &S
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FILING DATE: 1999-07-29
APPLICATION NUMBER: US 60/146,452
FILING DATE: 1999-07-29
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APPLICATION NUMBER: US 60/143,928
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LOCATION: 234174..234321
LOCATION: 234174..234321
COCATION: Exon O complement g34872
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LOCATION: 231787..231880
OTHER INFORMATION: exon (
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LOCATION: 229647..229742
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LOCATION: 215819..215975
LOCATION: exon
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NAME/KEY: exon
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TOCATION: 215819..215941
TOCATION: exon R
NAME/KEY: exon
LOCATION: 237406..237428
OTHER INFORMATION: exon Nbis complement g34872 gene
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LOCATION: 231272..231412
OTHER INFORMATION: exon Obis
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OTHER INFORMATION:
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LOCATION: 213818..215818
OTHER INFORMATION: 3'regulatory region g34872 gene
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LOCATION: 94124..94964
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LOCATION: 231870..231879
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LOCATION: 230408..230721
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OTHER INFORMATION: exon Q complement g34872 gene
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LOCATION: 216661..216952
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OTHER INFORMATION:
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COCATION: 217027..217061
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OCATION: 215702..215746
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JOCATION: 216836..216915
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Best Local
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LOCATION: 241686..243685
OTHER INFORMATION: 5'regulatory
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LOCATION: 290652..292652
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LOCATION: 240800..240993
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LOCATION: 240528..241685
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LOCATION: 240528..240824
OTHER INFORMATION: exon !
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OTHER INFORMATION:
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OTHER INFORMATION: exon M1090
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LOCATION: 239719..239853
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COATION: 239719..239807
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LOCATION: 240528..240617
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ORMATION: exon M692 complement
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TATATAAATTATA-ATATATATAAATTATATATATACATATTTATAATATACACAATTT
                                                                                   GAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATTTCAA 1144
                                                                                                                                                                                               AAACCAACTGTTATGTTTTCTTTTCAGTGAGTTTATGGTAGTCTTTTAAAAATCACATTGG
                            СТТТСТАТТТСТТААТААААТGATTATTCAAGGAAAAAAAAAAAAAA 1193
                                                                                                                                                            TAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTGTA 1084
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Pred. No. 2
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US-10-750-185-36894/c
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LENGTH: 1443
TYPE: DNA
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CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIN version 3.1
SEQ ID NO 36894
LENGTH: 1301
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                                                                          Matches 104;
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Best Local Similarity
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APPLICANT:
APPLICANT:
APPLICANT:
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CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILLING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
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APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMI1100-2
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APPLICANT: DENISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
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APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
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                                    980 AAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATTAGACATGGTTGGGA 1039
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ROSENFELD, David
HOLM, Tom
AACCTAAGTGTCCATGACAGATGAACAGATAAAGAAAATGTGGAAAACACATACAATGGA
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Pred. No. 5.3;
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                                                                            Mismatches
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                                                                                                                 DB 6;
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GENERAL INFORMATION:
APPLICANT: WMI GENOMICS, INC.
APPLICANT: DENISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: KERR, Richard
APPLICANT: HOLM, Tom
APPLICANT: HOLM, Tom
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOY
FILE REFERENCE: MMII100-2
CURRENT APPLICATION MUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
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US-10-750-185-51935
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US-10-750-185-32077/c
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Best Local Similarity 53.0
Matches 79; Conservative
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SEQ ID NO 32077
LENGTH: 1495
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CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
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APPLICANT: DENISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
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APPLICANT: FANTIN, DENNIS
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMI1100-2
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Pred. No. 6.8;
0; Mismatches
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                                                                      BOVINE
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RESULT 11
US-10-750-185-51383/c
Sequence 51383, Application US/10750185
Publication No. US20050260603A1
GENERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.
APPLICANT: DENISE, Sue K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: DNA
; ORGANISM: Bovine
US-10-750-185-46765
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; SEQ ID NO 51935

; LENGTH: 1798

; TYPE: DNA

; ORGANISM: Bovine 19866880871

US-10-750-185-51935
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Best Local Similarity 52.6
Conservative
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Best Local Similarity 62.4%;
Matches 58; Conservative
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMI1100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: MMI GENOMICS, APPLICANT: DeNISE, Sue I APPLICANT: KERR, Richard
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PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1835
                                                                                                                                                                                          1442
                                                                                                                                                                                                                                                                                                                 1104 TTTTTGTTCAATATTGATATTTTATCACCAACATTTCAAGTTTGTATTTGTTAATAAA 1163
                                                                                                                                                                                                                                                                                                                                                                                               1044 GTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTGTAGAATTACTGTTTACACACA 1103
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                                                                                                                                                                                        AATATATTACTGGGAAAAGGTTAAAAAATAAA 1473
                                                                                                                                                                                                                            АТБАТТАТТСААББАААААААААААААА 1195
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KERR, Richard
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52.6%;
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Pred. No. 8.2;
0; Mismatches
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APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMIII00-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER: OF SEQ ID NOS: 64922
SOFTWARE: PAtentIN version 3.1
SEQ ID NO 51383
LENGTH: 2081
TYPE: DNA
ORGANISM: Bovine 19866880958299
US-10-750-185-51383
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RESULT 13
US-11-099-691-22
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US-10-750-185-52737/c
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US-10-750-185-52737
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SEQ ID NO 52737
LENGTH: 1620
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APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMI1100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR PILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
RUMBER OF SEQ ID NOS: 64922
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Local Similarity 57.4%;
nes 66; Conservative
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                                                                                                             1080 TTGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACAT 1139
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                                                                           TTATAGCAAAATTATTTTCCAGTATTTTTTTAAAAACTAGAGCTATTTTATAGGGGGATAC 286
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KERR, Richard
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Pred. No. 8.7;
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; LENGTH: 1577
; TYPE: DNA
; ORGANISM: Bovine
US-10-750-185-45671
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CURRENT APPLICATION NUMBER: US/11/099,691
CURRENT APPLICATION NUMBER: US/09/700,444
PRIOR APPLICATION NUMBER: US/09/700,444
PRIOR FILING DATE: 2002-08-26
PRIOR APPLICATION NUMBER: 60/085,343
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/098,010
PRIOR APPLICATION NUMBER: 60/098,010
PRIOR FILING DATE: 1998-08-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PERL Program
SEQ ID NO 22
LENGTH: 2948
                                                                                                         SOFTWARE: PatentIN version 3.1 SEQ ID NO 45671
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Publication No. US20050260644A1
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APPLICANT:
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APPLICANT: BANDMAN, Olga
APPLICANT: HILLMAN, Jennifer L.
Query Match
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APPLICANT: BAUGHN, Mariah R.
APPLICANT: YANG, Junming
TITLE OF INVENTION: CELL SIGNALING PROTEINS
FILE REFERENCE: PF-0521 PCT
                                                                                                                                                              APPLICANT: FANTIN, Definis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMII100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR PILING DATE: 2002-12-31
                                                                                                                                                                                                                                                                                                                                                        APPLICANT: MMI GENOMICS, INC. APPLICANT: DENISE, Sue K. APPLICANT: KERR, Richard
                                                                                                                                          PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION:
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YUE, Henry
TANG, Y. Tom
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BATES, Stephen
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                                                        19866880420845
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   3.0%; Score 36.2;
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Pred. No. 13
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   Length 1577;
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GENERAL INFORMATION:

APPLICANT: MMI GENOMICS, INC.

APPLICANT: DENISE, Sue K.

APPLICANT: KEER, Richard

APPLICANT: ROSENFELD, David

APPLICANT: HOLM, Tom

APPLICANT: HATES, Stephen

APPLICANT: PANTIN, Dennis

TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS

FILE REFERENCE: MMILLO-2

CURRENT APPLICATION NUMBER: US/10/750,185

CURRENT FILING DATE: 2003-12-31

PRIOR APPLICATION NUMBER: US 60/437,482

PRIOR FILING DATE: 2002-12-31

PRIOR FILING DATE: 2002-12-31

VOMBER OF SEQ ID NOS: 64922

SOFTWARE: PARECHIN Version 3.1

SEQ ID NO 42808

LENGTH: 1978
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; ORGANISM: Bovine 19866880681507
US-10-750-185-42808
Search completed: December 5, 2005, 08:05:49
Job time : 379.544 secs
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US-10-750-185-42808/c
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                                                                                        1509
                                                                                                           1569 GTATTTAAATCTCTGATTAATTTAAATCTTGCTCTATATTGACTTAAATTTGCTTTGAAA 1510
                                                                                                                                                                                                         1079 GTTGTAGAATTTACTGTTTACACACATTTTTTGTTCAATATTTGA--TATATTTTTTATCACCAA 1136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1042 АТАТАТАТАТАТАТТАТАТТАСТАЛАТАЛАТДАЛ ПОВ СТАТАЛА ПОВ 1098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1072 GTTCCCAGTTGTAGAATTACTGTTTACACACACTTTTTGTTCAATATTTGATATATTTTATC 1131
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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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ALIGNMENTS

δ 밁 S 밁 Ś ₽ δ US-09-323-873A-1 US-09-323-873A-1 GENERAL INFORMATION: PRIOR APPLICATION NUMBER: 60/087,520 PRIOR FILING DATE: 1998-06-01 PRIOR APPLICATION NUMBER: 60/091,183 PRIOR FILING DATE: 1998-06-30 NUMBER OF SEO ID NOS: 32 SOFTWARE: FastSEQ for Windows Version SEQ ID NO 1 Query Match Best Local Sequence 1, Application US/09323873A Patent No. 6329503 Matches APPLICANT: Daniel E. Afar APPLICANT: Rene S. Hubert APPLICANT: Kahan Leong APPLICANT: Kahan Leong APPLICANT: Douglas C. Saffran APPLICANT: Douglas C. Saffran APPLICANT: Steve Chappell Micchell TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THE FILE REFERENCE: 129.16USUZ CURRENT APPLICATION NUMBER: US/09/323,873A CURRENT FILING DATE: 1999-06-01 LENGTH: 1195 TYPE: DNA ORGANISM: Homo Sapiens 1195; 181 121 121 61 61 AATTAATGGAAAGCAGAAAAGÁCÁTCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTATAG h 100.0%; Score 1195; DB 3; Similarity 100.0%; Pred. No. 6.6e-301; 95; Conservative 0; Mismatches 0; AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCCAGCATGCTAA 180 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAAGAACTTTGGAAAATGAAGCCTA 120 AND USES THEREOF Indels Length 1195; 0, Gaps

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APPLICANT: Harlocker, Susan L.
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Li, Samuel
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
APPLICANT: DIAGNOSIS OF PROSTATE CAL
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CAL
TITLE REFERENCE: 210121.427021
CURRENT APPLICATION NUMBER: US/09/685,166A
CURRENT FILING DATE: 2000-10-10
NUMBER OF SEO ID NOS: 898
SOFTWARE: FRASTSEQ for Windows Version 3.0
SEO ID NO 878
LENGTH: 1195
TYPE: DNA
ORGANISM: Homo sapiens
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Pred. No. 6.6e-301;
; Mismatches 0;
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US-09-679-426-878

Sequence 878, Application US/09679426

Patent No. 6759515

GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Kalos, Michael D.
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Li, Samuel
APPLICANT: Li, Samuel
APPLICANT: Li, Samuel
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE C.
FILE REFERENCE: 210121.427C20
CURRENT FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 895
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 878
LENGTH: 1195
LENGTH: 1195
TYPE: DNA
ORGANISM: Homo
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APPLICANT: Wang, Aijun
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THE
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C23
CURRENT APPLICATION NUMBER: US/09/759,143
CURRENT FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 934
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 878
LENGTH: 1195
TYPE: DNA
ORGANISM: Homo sapiens
US-09-759-143-878
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Patent No. 6800746
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Mitcham, Jenni
APPLICANT: Mitcham, Jenni
APPLICANT: Harlocker, Sus;
APPLICANT: Jiang, Yuqni
APPLICANT: Henderson, Rob
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US-09-759-143-878
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Best Local Similarity
Matches 1195; Conserv
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Fanger, Gary R.
Retter, Marc W.
Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
                                  CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Samuel
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Sequence 1, Application US/10010667A

Patent No. 6887975

GENERAL INFORMATION:

APPLICANT: Afar, Daniel

APPLICANT: Hubert, Rene S.

APPLICANT: Leong, Kahan

APPLICANT: Raitano, Arthur B.

APPLICANT: Raitano, Douglas C.

APPLICANT: Mitchell, Steve Chappell

TITLE OF INVENTION: NOVEL SERPENTINE TH
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US-10-010-667A-1
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; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-010-667A-1
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FILE REFERENCE: 511582001601
CURRENT APPLICATION NUMBER: US/10/010,667A
CURRENT FILLING DATE: 2001-12-06
PRIOR APPLICATION NUMBER: 09/323,873
PRIOR FILLING DATE: 1999-06-01
PRIOR APPLICATION NUMBER: 60/087,520
PRIOR APPLICATION NUMBER: 60/087,520
PRIOR APPLICATION NUMBER: 60/087,520
PRIOR APPLICATION NUMBER: 60/091,183
PRIOR APPLICATION NUMBER: 60/091,183
PRIOR FILLING DATE: 1998-06-30
PRIOR FILLING DATE: 1998-06-30
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SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 1
LENGTH: 1195
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                                       APPLICANT: Meagher, Madaliane Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C27
CURRENT APPLICATION NUMBER: US/10/012,896
CURRENT FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 1011
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 878
LENGTH: 1195
TYPE: DNA
ORGANISM: Homo sapiens
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APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqiu
APPLICANT: Kalos, Michael D.
                               US-10-012-896-878
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Query Match
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Patent No. 694323
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Houghton, Raymond L.
Vinals de Bassols, Carlota
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Hepler, William T.
Henderson, Robert A.
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Vedvick, Thomas S.
Carter, Darrick
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Kalos, Michael D.
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APPLICANT: Daniel E. Afar
APPLICANT: Rene S. Hubert
APPLICANT: Arthur B. Raitano
APPLICANT: Arthur B. Raitano
APPLICANT: Douglas C. Saffran
APPLICANT: Stephen C. Mitchell
TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
TITLE OF INVENTION: NOVEL SERVENTINE TRANSMEMBRANE ANTIGENS
TITLE OF INVENTION: NOVEL SERVENTINE TRANSMEMBRANE ANTIGENS
TITLE OF INVENTION: 199-17-08
CURRENT APPLICATION NUMBER: US/09/455,486
CURRENT FILING DATE: 1999-12-06
PRIOR APPLICATION NUMBER: 09/23,873
PRIOR FILING DATE: 1999-06-01
NUMBER OF SEG ID NOS: 34
COPTUMBER: FRANCE OF WINDOWS Version 4.0
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LENGTH: 1193
TYPE: DNA
ORGANISM: HOMO
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NAME/KEY: CDS
LOCATION: (64)...(1083)
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/237,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 2686
LENGTH: 1147
TYPE: DNA
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US-09-949-016-2686
; Sequence 2686, Application US/09949016
; Patent No. 6812339
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Best Local Similarity
Matches 1144; Conserv
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Pred. No. 1.7e.
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CURRENT APPLICATION NUMBER: US/09/323,873A
CURRENT FILING DATE: 1999-06-01
PRIOR APPLICATION NUMBER: 60/087,520
PRIOR FILING DATE: 1998-06-01
PRIOR APPLICATION NUMBER: 60/091,183
PRIOR FILING DATE: 1998-06-30
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSEQ for Windows Version 4.0
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GENERAL INFORMATION:
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Best Local Similarity
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APPLICANT: Douglas C. Saifran
APPLICANT: Steve Chappell Mitchell
TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF
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APPLICANT: Rene S. Hubert
APPLICANT: Kahan Leong
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ORGANISM: Homo Sapiens
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Pred. No. 1.2e-204;
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APPLICANT: Daniel E. Afar
APPLICANT: Rene S. Hubert
APPLICANT: Rene S. Hubert
APPLICANT: Arthur B. Raitano
APPLICANT: Douglas C. Saffran
APPLICANT: Stephen C. Mitchell
TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF
FILE REFERENCE: 129.17-US-11
CURRENT APPLICATION NUMBER: US/09/455,486
CURRENT APPLICATION NUMBER: US/09/455,486
CURRENT FILING DATE: 1999-12-06
PRIOR APPLICATION NUMBER: 09/323,873
PRIOR FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PastSEQ for Windows Version 4.0
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SEQ ID NO 4
; LENGTH: 3627
; TYPE: DNA
; ORGANISM: Homo sapiens
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APPLICANT: Daniel
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Best Local Similarity 99.5%;
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Pred. No. 1.2e-204;
0; Mismatches 4;
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US-10-010-667A-6

Sequence 6, Application US/10010667A

Patent No. 6887975

GENERAL INFORMATION:
APPLICANT: Hubert, Rene S.
APPLICANT: Hubert, Rene S.
APPLICANT: Hubert, Rene S.
APPLICANT: Hubert, Rene S.
APPLICANT: Saftran, Douglas C.
APPLICANT: Mitchell, Steve Chappell
APPLICANT: Mitchell, Steve Chappell
TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
TITLE OF INVENTION: NUMBER: US/10/010,667A

CURRENT FILING DATE: 2001-12-06

PRIOR APPLICATION NUMBER: 09/323,873

PRIOR PILING DATE: 1999-06-01

PRIOR APPLICATION NUMBER: 60/087,520

PRIOR APPLICATION NUMBER: 60/087,520

PRIOR APPLICATION NUMBER: 60/091,183

PRIOR FILING DATE: 1998-06-30

NUMBER OF SEQ ID NOS: 32

SOFTWARE: PASTSEQ for Windows Version 4.0

LENGTH: 3627

TYPE: DNA
ORGANISM: Homo sapiens
US-10-010-667A-6
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                                              ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC
                                                                                                                                                   CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGGTAAA
                                    ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGACATCTATTC
                                                                         AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT
                                                                                  AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT
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99.5%;
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Pred. No. 1.2e-204;
0; Mismatches 4;
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RESULT 12
US-09-439-313-342/c
; Sequence 342, Application US/09439313
; Patent No. 6329505
; GENERAL INFORMATION:
; APPLICANT: Ni, Jiangchun
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yuqui
; APPLICANT: Reed, Steven G.
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US-09-352-616A-342/c
Sequence 342, Application US/09
Sequence 342, Application US/09
Patent No. 6395278
GENERAL INFORMATION:
APPLICANT: Dillon, Davin C.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqui
APPLICANT: Xu, Jiangchun
APPLICANT: Mitcham, Jennifer
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APPLICANT: Fenger, Gary
APPLICANT: Retter, Mark
APPLICANT: Solk, John
APPLICANT: Solk, John
APPLICANT: Day, Craig
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C9
CURRENT APPLICATION NUMBER: US/09/439,313
CURRENT APPLICATION NUMBER: US/09/439,313
CURRENT FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 575
SOFTWARE: PastSEQ for Windows Version 3.0
LENGTH: 592
TYPE: NNA
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Jiang, Yuqui
Xu, Jiangchun
Mitcham, Jennifer Lynn
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99.7%;
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TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS;
TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE;
FILE REFERENCE: 210121.427C8;
CURRENT APPLICATION NUMBER: US/09/352,616A;
CURRENT FILING DATE: 1999-07-13;
NUMBER OF SEQ ID NOS: 472;
SOFTWARE: FastSEQ for Windows Version 3.0;
SEQ ID NO 342;
TYPE: DNA 42;
ORGANISM: Homo Bapien
US-09-352-616A-342
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Best Local Similarity 99.7%;
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TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGT
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                                                  CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG
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                                 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG
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Pred. No. 2.6e-141;
1; Mismatches 1;
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RESULT 14

US-09-636-215-342/c

US-09-636-215-342/c

; Sequence 342, Application US/09636215
; Patent No. 6620922
; GENERAL INFORMATION:
; APPLICANT: Millon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fenger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.

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TAACAAGAAAGCARATTGGGCTTCTCAGTTTTCTTTTTGCTGT

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APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Wang, Aijun
APPLICANT: Hepler, William
ITILE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
ITILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
ITILE REFERENCE: 210121.42717017
CURRENT APPLICATION NUMBER: US/09/636,215
CURRENT APPLICATION NUMBER: US/09/636,215
CURRENT FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 852
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 342
LENGTH: 592
TYPE: DNA
ORGANISM: Homo Bapien
US-09-636-215-342
RESULT 15
US-09-685-166A-342/c
US-09-685-166A-342/c
; Sequence 342, Application US/0968; Patent No. 6630305; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun; APPLICANT: Mitcham, Jennifer L.; APPLICANT: Mitcham, Jennifer L.
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APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqui
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Marc W.
APPLICANT: Li, Samuel
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Weng, Aijun
APPLICANT: Hepler, William
ITILE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
ITILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C21
CURRENT APPLICATION NUMBER: US/09/685,166A
CURRENT APPLICATION DATE: 2000-10-10
NUMBER OF SEQ ID NOS: 898
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 342
LENGTH: 592
TYDE: DNA
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2: /cgn2=6/ptodata/1/pubpna/US08_PUBCOMB.seq:*

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US-10-011-095-1
US-10-010-667N-1
US-10-010-667N-1
US-10-144-678A-878
US-10-294-025-878
US-10-393-507-35
US-10-393-507-35
US-10-394-037-313
US-10-295-027-1130
US-10-643-795A-16
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Sequence 878, App
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Sequence 396, App
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Sequence 397, Appli
Sequence 378, App
Sequence 35, Appl
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Sequence 1130, App
Sequence 1130, App
Sequence 1130, Appl
Sequence 115, Appl
Sequence 16, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 18, Appl
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69.1	69.1	69.2	69.2	87.7	87.7	97.6	98.5	98.5	98.6	98.9	98.9	99.8	99.8	99.8	99.8	99.8	99.8	100.0	100.0	100.0	100.0
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Sequence 6, App.	Sequence 6, Appl	Sequence 10, App	Sequence 10, App	Sequence 6, Appl:	Sequence 6, Appli	Sequence 5120, A	Sequence 16445, 1	Sequence 15, Appl		Sequence 2, Appli	Sequence 2, Appl:	Sequence 1, Appli	Sequence 1, Appl:	Sequence 1, Appl	Sequence 1, Appl:	Sequence 1, Appl:	Sequence 1, Appl	Sequence 191, App	Sequence 396, App	Sequence 428, App	Sequence 1, Appli

ALIGNMENTS

GENERAL INFO APPLICANT RESULT 1 US-09-759-143-878 Sequence 878, Application US/09759143 Patent No. US20020022248A1 TITLE INFORMATION: T: Wang, Aijun T: Keiky, Yasir A.W. T: Hepler, William INVENTION: COMPOSITIONS INVENTION: DIAGNOSIS OF Henderson, Robert Kalos, Michael D. Fanger, Gary R. Retter, Marc W. Stolk, John A. Day, Craig H. Vedvick, Thomas S. Carter, Darrick Jiang, Yuqui Mitcham, Jennifer Harlocker, Susan I Xu, Jiangchun Dillon, Davin Li, Samuel Robert A. ი D. . . AND METHODS FOR THE THERAPY AND PROSTATE CANCER

Db	γQ	Db	γQ	Matches	Query Match	US-09-759-143-878	; ORGAI	; TYPE: DNA	; LENG:	; SEQ ID NO 878	; SOFTW	; NUMBEI	; CURREI	; CURREI	; FILE I	; TITLE
61 AATTAATGGAAAGCAGAAAGACATCACAAACCCAAGAAGAACTTTGGAAAATGAAGCCTA	61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 1	1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG	1 CCGAGACTCACGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG	Matches 1195; Conservative 0; Mismatches 0; Indels 0; Gaps		1-143-878	ORGANISM: Homo sapiens	DNA	LENGTH: 1195	NO 878	SOFTWARE: FastSEQ for Windows Version 3.0	NUMBER OF SEQ ID NOS: 934	CURRENT FILING DATE: 2001-01-12	CURRENT APPLICATION NUMBER: US/09/759,143	FILE REFERENCE: 210121.427C23	TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

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APPLICANT: MCNeil), Patricia D.
APPLICANT: HOUGHLON, RAYMOND L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: COMPOSITIONS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C24
CURRENT APPLICATION NUMBER: US/09/780,669
CURRENT FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 943
SOFTWARE: FRASESEQ for Windows Version 3.0
SEQ ID NO 878
LENGTH: 1195
TYPE: DNA
ORGANISM: Homo sapiens
US-09-780-669-878
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US-09-780-669-878
Sequence 878, Application US
Sequence 878, Application US
Patent No. US20020051977A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C
APPLICANT: Hitcham, Jennif
APPLICANT: Harlocker, Susa
APPLICANT: Harlocker, Susa
APPLICANT: Henderson, Robe
APPLICANT: Henderson, Robe
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Retter, Marc W.
APPLICANT: Day, Craig H.
APPLICANT: Uedvick, Thomas
APPLICANT: Carter, Darrick
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Retter, Marc W.
Stolk, John A.
Day, Craig H.
Vedvick, Thomas S
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Hepler, William
Hural, John
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Vedvick, Thomas
Carter, Darrick
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Dillon, Davin C.
Mitcham, Jennifer
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RESULT 3

US-09-822-827-878

(Sequence 878, Application US/09822827

Patent No. US20020081680A1

(GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCE
FILE REFERENCE: 210121.534C1

(CURRENT APPLICATION NUMBER: US/09/822,827

(CURRENT FILING DATE: 2001-03-28

NUMBER OF SEQ ID NOS: 982

(SOFTWARE: FRASTSEQ for Windows Version 3.0

(SEQ ID NO 878
LENGTH: 1195
TYPE: DNA

(ORGANISM: Homo sapiens

US-09-822-827-878
Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 1195; Conservative 0
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Score 1195; DB 3;
Pred. No. 1.1e-281;
Mismatches 0;
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             AGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT
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APPLICANT: FOY, Teresa
APPLICANT: Fanger, Gary R.

APPLICANT: Fanger, Gary R.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THE
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.534C2
CURRENT APPLICATION NUMBER: US/09/895,793
CURRENT FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 982
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 878
LENGTH: 1195
TYPE: DNA
ORGANISM: Homo sapiens
US-09-895-793-878
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Publication No. US20020192763A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 1195; Conserv
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Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
Li, Samuel X.
Wang, Aijun
Skeiky, Yasir A.W.
Hepler, William T.
Henderson, Robert A.
                                  CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG
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                  CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG
                                                                           APAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT
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McNeill, Patricia D.
Houghton, Raymond L.
Vinals de Bassols, Carlota
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Kalos, Michael D.
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 Sequence 878, Application US/098958
Publication No. US20020193296A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqiu
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
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US-09-895-814-878
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Jiang, Yuqiu
Kalos, Michael D.
Retter, Marc W.
                                                                                                                    Application US/09895814 o. US20020193296A1
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APPLICANT: Fanger, Gary R.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THE TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER FILE REFERENCE: 210121.427C26

CURRENT APPLICATION NUMBER: US/09/895,814

CURRENT FILING DATE: 2001-06-29

NUMBER OF SEQ ID NOS: 990

SOFTWARE: FASTSEQ for Windows Version 3.0

SEQ ID NO 878

LENGTH: 1195

TYPE: DNA

ORGANISM: Homo Bapiens

US-09-895-814-878
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Best Local Similarity
Matches 1195; Conserv
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McNeill, Patricia D.
Houghton, Raymond L.
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Hepler, William T.
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Vedvick, Thomas
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Pred. No. 1.1e-281;
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Publication No. US20020183251AI
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Miccham, Jennifer
APPLICANT: Harlocker, Susan I
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            APPLICANT: Fanger, Gary R.
APPLICANT: Wantanabe, Yoshihiro
APPLICANT: Meagher, Madeleine Joy
APPLICANT: Meagher, Madeleine Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C27
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Vedvick, Thomas
Carter, Darrick
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McNeili, Patricia D.
McNeili, Patricia D.
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Foy, Teresa
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Hepler, William T.
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Kalos, Michael D.
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; CURRENT FILING DATE: 2001-12-10; NUMBER OF SEQ ID NOS: 1011; SOFTWARE: FastSEQ for Windows Version 3.; SEQ ID NO 878; LENGTH: 1195; TYPE: DNA; ORGANISM: Homo sapiens US-10-012-896-878
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                                                                                     ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC
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TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG

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GENERAL INFORMATION:

APPLICANT: Afar, Daniel
APPLICANT: Hubert, Rene S.
APPLICANT: Leong, Kahan
APPLICANT: Leong, Kahan
APPLICANT: Raitano, Arthur B.
APPLICANT: Mitchell, Steve Chappell
TITLE OF INVENTION: ANTIBODIES IMMUNOSPECIFIC FOR STEAP1 (AS AMENDED)
FILE REFERENCE: 511582001610
CURRENT FILING DATE: 1090-06-01
CURRENT FILING DATE: 1090-06-01
PRIOR APPLICATION NUMBER: 60/087,520
PRIOR FILING DATE: 1998-06-01
PRIOR APPLICATION NUMBER: 60/087,520
PRIOR FILING DATE: 1998-06-03
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1195
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Matches 1195;
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Publication No. US20030045682A1
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CAGAACTTCAGCACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG
                CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG
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RESULT 8
US-10-010-667A-1
US-10-010-667A-1
Sequence 1, Application US/10010667A
publication No. US20030055217A1
GENERAL INFORMATION:
APPLICANT: Afar, Daniel
APPLICANT: Hubert, Rene S.
APPLICANT: Leong, Kahan
APPLICANT: Raitano, Arthur B.
APPLICANT: Saffran, Douglas C.
APPLICANT: Mitchell, Steve Chappell
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; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-010-667A-1
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TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREO
FILE REFERENCE: 511582001601
CURRENT APPLICATION NUMBER: US/10/010,667A
CURRENT FILING DATE: 2001-12-06
PRIOR APPLICATION NUMBER: 09/323,873
PRIOR FILING DATE: 1999-06-01
PRIOR APPLICATION NUMBER: 60/087,520
PRIOR FILING DATE: 1998-06-01
PRIOR APPLICATION NUMBER: 60/091,183
PRIOR FILING DATE: 1998-06-30
NUMBER OF SEQ ID NOS: 32
SOPTMARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1195
TYPE: DNA

Query Match 100.0%; Score 1195; DB 5; Best Local Similarity 100.0%; Pred. No. 1.1e-281; Matches 1195; Conservative 0; Mismatches 0; Indels Length 0 Gaps

CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA AATTAATGGAAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120 240 180 180 120 60 0

CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG

CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420 420 360

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NUMBER SOFTWAN SEQ ID LENG: TYPE TYPE ORGAN S-10-20: Query N Best Lo	PRIOR FILING DATE: 2001-09-25 ; PRIOR APPLICATION NUMBER: 60/341,746 ; PRIOR APPLICATION NUMBER: 60/362,158 ; PRIOR APPLICATION NUMBER: 60/362,158 ; PRIOR FILING DATE: 2002-03-05		TILLE OF INVENTION: INDEATE OF FILE REFERENCE: MRI-044 CURRENT APPLICATION NUMBER: US/1 CURRENT FILING DATE: 2002-07-25	TI		APPLICANT: APPLICANT: APPLICANT:	publication N GENERAL INFOR APPLICANT: S	to Ht	Qy 1141 TCAAGTTTGTATTTGTATAAAAAAAATGATTATTCAAGGAAAAAAAA	QY 1081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATT 1140	QY 1021 AGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT 1080	QY 961 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1020	Qy 901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCC	Qy 841 TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 900	Qy 781 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840	Db 721 ATGTGTCTCTGGGAATTGTGGGAATACTGGCTCTGTTGGCTGTGACATCTATTC 780
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APPLICANT: Watanabe, Yoshihiro
APPLICANT: Deng, Ta
APPLICANT: Deng, Ta
ITILE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THE
ITITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
ITILE REFERENCE: 210121.427C28
CURRENT APPLICATION NUMBER: US/10/144,678A
CURRENT FILING DATE: 2002-08-12
NUMBER OF SEQ ID NOS: 1033
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 878
LENGTH: 1195
TYPE: DUA
ORGANISM: Homo sapiens
US-10-144-678A-878
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US-10-144-678A-878
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Publication No. US20030157089A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
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Best Local Similarity
Matches 1195; Conserv
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Hepler, William T.
Hural, John
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Kalos, Michael D.
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                                                                                                                                                                                                                                                         100.0%; Score 1195; DB 6; llarity 100.0%; Pred. No. 1.1e-281; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thomas S
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                                                       Sequence 878, Applic Publication No. US20 GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Stolk, John A.
APPLICANT: Kalos, Michael D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS
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; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE (
FILE REFERENCE: 2.10121.427C29
; CURRENT APPLICATION NUMBER: US/10/294,025
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEO ID NOS: 1038
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 878
; ENGTH: 1195
; TYPE: DUA
; ORGANISM: Homo sapiens
US-10-294-025-878
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Best Local Similarity
Matches 1195; Conserv
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APPLICANT: WANG, YIXIN

TITLE OF INVENTION: BREAST CANCER PROGNASTIC POI

FILE REFERENCE: CDS 268 US NP

CURRENT APPLICATION NUMBER: US/10/393,590

CURRENT FILING DATE: 2003-03-21

PRIOR APPLICATION NUMBER: 60/368,789

PRIOR FILING DATE: 2002-03-29

NUMBER OF SEQ ID NOS: 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: DNA ; ORGANISM: human US-10-393-590-35
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SEQ ID NO 35
LENGTH: 1195
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Publication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 1195;
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Best Local Similarity
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No. US20030190656A1
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ilarity 100.0%;
Conservative 0
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Pred. No. 1.1e-281;
0; Mismatches 0;
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RESULT US-10-3 SEGUEN GENER APEL TITIL TITIL CURR CURR CURR CURR CURR CURR CURR CUR	8 8 8 8	B & B &	D 64 B	8 8 8	9 da 64	Oy Db	& B &	Qy Db
RESULT 13 US-10-393-567-35 (Sequence 35, Application US/10393567) Sequence 35, Application US/10393567 Sequence 35, Application US/2030194733A1 GENERAL INFORMATION: APPLICANT: WANG, YIXIN FITLE OF INVENTION: CANCER DIAGNOSTIC PANEL FILE REFERENCE: CDS 269 US NP CURRENT APPLICATION NUMBER: US/10/393,567 CURRENT FILING DATE: 2003-03-21 PRIOR APPLICATION NUMBER: 60/368,667 PRIOR FILING DATE: 2002-03-29 NUMBER OF SEQ ID NOS: 100 SOFTWARE: PATINT NOS: 100 SOFTWARE: PATINT VETSION 3.1 SEQ ID NO 35 LENGTH: 1195	1081 TGTAGAATTACTGTTTACACACATTTTTGTTCAAGATATATTTTATCACCAACATT 1140 1081 TGTAGAATTACTGTTTACACACACATTTTTGTTCAATATTGATATATTTTTATCACCAACATT 1140 1141 TCAAGTTTGTATTTGTTAATAAAATGATTTATTCAAGGAAAAAAAA		TIGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTTGCCTGGAATAAGTGGATAGATA	CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA	661 AGGTCCAACAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT 720	541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTTGCTGTACTGCAGTTTATA 600 601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660 [481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGG	
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721 ATGUST CUCUSANT IN JUSTICAL LIGHT CONTROLL CONTROL CONTR	601 GTCTGTCTTACCCAATGAGGGATCCTACAGATACAGGTGATCTAGACTGGGCATATCAACTGGGCATATCAACTGGGCATATCAACTGGGCATATCAACTGGGCATACTAGATGAGGTTGATAACTGGGCATATCAACTGGGCATATCAACTGGGCATATCAACTGGGCATATCAACTGAGTTGAGAATGGAGAATGGAGATTGAGCATGATGTTTGGAGAATGGAGATTTTGAGAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTTGGAGAATGGAGATTTTTGAGAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTTGGAGAATTGAGAGATTTTGAGCATGATGTTTTGAGAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTTGAGAAATGGAGATTTTGAGCATGATGATGATGATGATGAGAATTGAGAGATTTTGAGCATGATGATGATGAGAATTGAGAGATTTTGAGCATGATGATGATGAGAATTGAGAGATTTTGAGCATGATGATGATGATGATGAGAGATTTTGAGAGAATTGAGAGATTTTGAGCATGATGATGATGATGATGATGATGAGAGATTTTGAGCATGATGATGATGATGATGATGAGAGATTTTTGAGCATGATGATGATGATGATGATGATGATGATGATGATGATGA			301 CTATTATAGCATCTCTGACCTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG	181 AAAGACCTGTGCTTTTGCAGTTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT	61 AATTAATGGAAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 11	1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG	ANISM: human 93-567-35 Match 100.0%; Score 1195; DB 6; Length 1195; Local Similarity 100.0%; Pred. No. 1.1e-281; es 1,95; Conservative 0; Mismatches 0; Indels 0; Gaps

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Sequence 35, Application US/10394087
Publication No. US20030194734A1
GENERAL INFORMATION:
APPLICANT: Jatkoe, Tim
APPLICANT: Jatkoe, Tim
FILE OF INVENTION: SELECTION OF MARKERS
FILE REFERENCE: CDN 265 US NP
CURRENT APPLICATION NUMBER: US/10/394,087
CURRENT FILING DATE: 2003-03-21
PRIOR APPLICATION NUMBER: 60/368,790
PRIOR PILING DATE: 2003-03-29
NUMBER OF SEQ ID NOS: 100
SOFTWARE: PatentIn version 3.1
SEQ ID NO 35
LENGTH: 1195
TYPE: DNA
ORGANISM: human
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US-10-394-087-35
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Best Local Similarity
Matches 1195; Conser
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CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG
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100.0%; Pred. No. 1.1e-281;
tive 0; Mismatches 0;
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 APPLICANT: Murray, Nachard
APPLICANT: Murray, Richard
APPLICANT: Mateon, Susan R.
APPLICANT: Eos Biotechnology, Inc.
APPLICANT: Eos Biotechnology, Inc.
TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and TITLE OF INVENTION: Methods of Screening for Modulators of Cancer FILE REFERENCE: 018501-012500US
CURRENT APPLICATION NUMBER: US/10/295,027
CURRENT FILING DATE: 2002-11-13
PRIOR APPLICATION NUMBER: US 09/663,733
PRIOR APPLICATION NUMBER: US 60/350,666
PRIOR FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US 60/350,666
PRIOR APPLICATION NUMBER: US 60/35,394
PRIOR APPLICATION NUMBER: US 60/35,394
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US-10-295-027-713
                                                                                                                                                                                                                                                                    APPLICANT: Afar, Daniel
APPLICANT: Aziz, Natasha
APPLICANT: Ginsberg, Wendy
APPLICANT: Ginsberg, Con
APPLICANT: Glynne, Richard
APPLICANT: Hevezi, Peter A
                                                                                                                                                                                                                                                                                                                                                                       Sequence 713, Application US/10295027
Publication No. US20030232350A1
GENERAL INFORMATION:
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Glynne, Richard
Hevezi, Peter A.
Mack, David H.
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Gish, Kurt C.
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-295-027-713
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PRIOR FILING DATE: 2001-11-21
PRIOR PILING DATE: 2001-11-29
PRIOR PILING DATE: 2001-11-29
PRIOR PILING DATE: 2001-12-14
PRIOR FILING DATE: 2001-12-14
PRIOR PILING DATE: 2001-12-14
PRIOR APPLICATION NUMBER: US 60/347,211
PRIOR PILING DATE: 2002-01-08
PRIOR PILING DATE: 2002-01-10
PRIOR PILING DATE: 2002-01-10
PRIOR APPLICATION NUMBER: US 60/347,349
PRIOR PILING DATE: 2002-02-08
PRIOR PILING DATE: 2002-02-09
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PRIOR PILING DATE: 2002-02-08
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Best Local Similarity
Matches 1195; Conserv
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                                                              GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC
                                                                                         GTCTGTCTTACCCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACCTGGGCATATCAAC
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F	TCAAGTTTGTTAATAAATGATTATTCAAGGAAAAAAAAAA	1141	δ 8
1140	TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTTATCACCAACACTT	1081	3 8
1080	AGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT	1021	ф
1080	AGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT	1021	Qγ
1020	TTGTTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA	961	Db
1020	TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA	961	γQ
960	ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCC	901	Ъ
960		901	Ş
900	TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG	841	В
900	TTTGCCTGGAATAAGTGGATAG	841	γQ
840	CATCTGTGAGTGACTCTTTGACATGGAGAGATTTCACTATATTCAGAGCAAGCTAGGAA	781	ф
840	-	781	δ
780	ATGTGTCTCTGGGAATTGTGGGAATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC	721	ф
780	ATGTGTCTCTGGGAATTGTGGCAATACTGGCTCTGTTGGCAATATCC	721	ş
720	AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT	661	Вb

Search completed: December Job time: 1120.59 secs 5 2005, 07:54:08 Pris Prisologia Champe (USO)

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Result
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-Q=/G9n2_1/USPTO_spool h/US1075062/runat 06122005_162947_15675/app_query.fasta_1.519
-DBs-Published_Applications_NA_Main_OPMT=Fastap_SUFFIX=rnpbm_-MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS-bIts -START=1 =END=-1 -MATRIX=bLosun62
-TRANS=human40.cdi -LIST=45 -DCCALIGN=200 -THR_SCORE=pCt -THR_MXX=100
-THR_MIN=0 -ALIGN=15 -MODB=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US10750262 @CGN 1 1026 @runat 06122005_162947_15675
-NCPU=6 -LOUPL3 -NO_MAAP -LARGEQUERY -NGEG_SCORES=0 -WAIT_-DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-PGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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// cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
// cgn2_6/ptodata/1/pubpna/US098_PUBCOMB.seq:*
// cgn2_6/ptodata/1/pubpna/US108_PUBCOMB.seq:*
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       US-10-696-639-15

US-10-165-044-1

US-10-168-009-1

US-10-887-785-1

US-10-856-109-1

US-10-830-899-2

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equence 6, Appl	quence 6,	equence 6, Appl	equence 1300. A	equence 5120. A	equence	equence 6, Appl	equence 191, Ap	equence 199	equence 164	Sequence 39	equence 428	equence 1,	equence 704	equence 181	equence 42,	equence 16,	equence 1,	equence 42,	equence 16.	equence 113	equence 713	equence 35.	equence 35.	e 35	equence 878	equence 876	equence 396	emience 1	equence 1.	equence 878	equence 878	equence 87	equence 87	quence 878. Ap	equence 878.	equence 2. Annl

ALIGNMENTS

RESULT 1 US-10-696-639-15

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US-10-750-262-2 (1-339) x US-10-696-639-15 (1-1177)	Alignment Scores: Pred. No.: Score: Percent Similarity: Best Local Similarity: Query Match: DB:	Sequence 15, Application US/1069639 Publication No. US20050037439A1 GENERAL INFORMATION: APPLICANT: Pharmacia Corporation APPLICANT: Pharmacia Corporation APPLICANT: Bourner, Maureen J. TITLE OF INVENTION: DIERENTIALLY EXPRESSED GENES INVOLVED IN CANCER, THE TITLE OF INVENTION: DOLYPEPTIDES ENCODED THEREBY, AND METHODS OF USING THE SAME FILE REFERENCE: 0.0040/1 CURRENT APPLICATION NUMBER: US/10/696,639 CURRENT FILING DATE: 2003-10-29 PRIOR APPLICATION NUMBER: 60/422,176 PRIOR FILING DATE: 2002-10-29 NUMBER OF SEQ ID NOS: 3114 SOOTWARE: Patentin version 3.1 SEQ ID NO 15 LENGTH: 1177 TYPE: DNA ORGANISM: homo sapiens
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RESULT 2
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; Publication No. US20030149531A1
; GENERAL INFORMATION:
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APPLICANT: Rene S. Hubert
APPLICANT: Arthur B. Raitano
APPLICANT: Douglas Saffran
APPLICANT: Daniel E.H. Afar
APPLICANT: Steven Chappell Mitchell
APPLICANT: Mary Faris
APPLICANT: Mary Faris
APPLICANT: Aya Jakobovits
TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF
FILE REFERENCE: 51158-20016.02
CURRENT APPLICATION NUMBER: US/10/165,044
CURRENT FILING DATE: 2002-06-06
CURRENT FILING DATE: 2002-06-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 60/087,520
PRIOR FILING DATE: 1998-06-01
PRIOR FILING DATE: 1998-06-01
PRIOR APPLICATION NUMBER: US 60/091,183
PRIOR APPLICATION NUMBER: US 09/323,873
PRIOR APPLICATION NUMBER: US 09/455,486
PRIOR FILING DATE: 1999-06-01
PRIOR PILING DATE: 1999-12-06
PRIOR APPLICATION NUMBER: US 09/455,486
PRIOR PILING DATE: 1999-12-06
PRIOR PILING DATE: 1999-12-06
PRIOR PILING DATE: 1999-06-01
PRIOR PILING DATE: 1999-06-01
PRIOR FILING DATE: 1999-06-01
PRIOR FILING DATE: 2000-12-06
NUMBER OF SEQ ID NOS: 57
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1193
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APPLICANT: Daniel E. Afar
APPLICANT: Arthur B. Raitano
APPLICANT: Douglas C. Saffran
APPLICANT: Douglas C. Saffran
APPLICANT: Douglas C. Saffran
APPLICANT: Stephen C. Mitchell
TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREO
FILE REFERENCE: 511582001603
CURRENT APPLICATION NUMBER: US/10/408,009
CURRENT APPLICATION NUMBER: 09/455,486
PRIOR APPLICATION NUMBER: 09/455,486
PRIOR APPLICATION NUMBER: 09/323,873
PRIOR APPLICATION NUMBER: 09/323,873
PRIOR FILING DATE: 1999-12-06
PRIOR APPLICATION NUMBER: 09/323,873
PRIOR FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1193
TYDE: NOA
              Alignment Scores: Pred. No.:
                                                         US-10-408-009-1
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US-10-408-009-1
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                                                                                                 TYPE: DNA
ORGANISM: Homo
FEATURE:
                                                                   NAME/KEY: CDS
LOCATION: (64)...
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CURRENT APPLICATION NUMBER: US/10/857,785
CURRENT FILING DATE: 2004-05-28
ENTOR APPLICATION NUMBER: US 09/455,486
PRIOR FILING DATE: 1999-12-06
PRIOR FILING DATE: 1999-06-01
PRIOR FILING DATE: 1999-06-01
PRIOR APPLICATION NUMBER: US 60/087,520
PRIOR FILING DATE: 1998-06-01
PRIOR FILING DATE: 1998-06-30
NUMBER OF SEQ ID NOS: 47
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; LOCATION: (64)...(1083)
US-10-857-785-1
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Publication No. US20040219162A1
GENERAL INFORMATION:
APPLICANT: Daniel E. Afar
APPLICANT: Rene S. Hubert
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SEQ ID NO 1
LENCTH: 1193
TYPE: DNA
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APPLICANT: Arthur B. Raitano
APPLICANT: Douglas C. Saffran
APPLICANT: Stephen C. Mitchell
TITLE OF INVENTION: EXPERSISED IN HUMAN CANCERS AND USES THE
FILE REFERENCE: 511582001607
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US-10-856-109-1
Sequence 1, Application US/10856109
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; Sequence 1, Application US/10856109
; Publication No. US20040219591A1
; GENERAL INFORMATION:
 APPLICANT: Daniel E. Afar
 APPLICANT: Daniel E. Hubert
 APPLICANT: Deniel E. Hubert
 APPLICANT: Douglas C. Saffran
 APPLICANT: Stephen C. Mitchell
 TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF
 FILLE REFERENCE: 511582001606
 CURRENT APPLICATION NUMBER: US/10/856,109
 CURRENT FILING DATE: 1999-10-06
 PRIOR APPLICATION NUMBER: US 09/455,486
 PRIOR APPLICATION NUMBER: US 09/455,486
 PRIOR APPLICATION NUMBER: US 09/323,873
 PRIOR APPLICATION NUMBER: US 09/323,873
 PRIOR APPLICATION NUMBER: US 60/087,520
 PRIOR FILING DATE: 1998-06-30
 NUMBER OF SEQ ID NOS: 47
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 1
 LENGTH: 1193
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: CDS

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                                           SerLeuLeuGlyThrIleHisAlaLeuIlePheAlaTrpAsnLysTrpIleAspIle
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 AMACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTTCCAATTGTT
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APPLICANT: Gudas, Dean
APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICATION: therefrom that Bind to STEAP-1 Prot
FILE REFERENCE: 51158-20016.26
CURRENT APPLICATION NUMBER: US/10/830,899
CURRENT FILING DATE: 2004-04-23
PRIOR APPLICATION NUMBER: 09/323,873
PRIOR APPLICATION NUMBER: 10/010,667
PRIOR APPLICATION NUMBER: 10/010,667
PRIOR FILING DATE: 2001-12-06
PRIOR APPLICATION NUMBER: 10/011,095
PRIOR APPLICATION NUMBER: 10/236,878
PRIOR APPLICATION NUMBER: 09/455,486
PRIOR FILING DATE: 1998-06-30

NUMBER OF SEQ ID NOS: 103
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 1193
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US-10-830-899-2
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APPLICANT: Jakobovits, Aya
APPLICANT: Etessami, Soudabeh
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Perez-Villar, Juan
APPLICANT: Meyrick Morrison, Karen
APPLICANT: Jia, Xiao-Chi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/10830899 Publication No. US2004025323232A1
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ORGANISM: Homo
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LOCATION: (66)...
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                                       CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA
                                                               LeuGlnHisThrGlnGluLeuPheProGlnTrpHisLeuProIleLysIleAlaAlaIle
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Gudas, Jean
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APPLICANT: Agensys, Inc.
APPLICANT: Rene S. Hubert
APPLICANT: Arthur B. Raitano
APPLICANT: Douglas Saffran
APPLICANT: Douglas Saffran
APPLICANT: Daniel E.H. Afar
APPLICANT: Steven Chappell Mitchell
APPLICANT: Mary Faris
APPLICANT: Mary Faris
TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREO
FILE REFERENCE: 51158-20016.02
CURRENT APPLICATION NUMBER: US/10/753,195
CURRENT FILING DATE: 2004-01-06
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Best Local Similarity:
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PRIOR FILING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: US 60/087,520
PRIOR FILING DATE: 1998-06-01
PRIOR APPLICATION NUMBER: US 09/323,873
PRIOR APPLICATION NUMBER: US 09/323,873
PRIOR APPLICATION NUMBER: US 09/455,486
PRIOR FILING DATE: 1999-06-01
PRIOR APPLICATION NUMBER: US 09/455,486
PRIOR APPLICATION NUMBER: US 09/45941
PRIOR APPLICATION NUMBER: WO 99/62941
PRIOR PILING DATE: 1999-12-06
PRIOR PILING DATE: 1999-12-06
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LOCATION: (64)
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GENERAL INFORMATION:
APPLICANT: Daniel E. Afar
APPLICANT: Rene S. Hubert
APPLICANT: Arthur B. Raitano
APPLICANT: Douglas C. Saffran
APPLICANT: Stephen C. Mitchell
TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
TILE REFERENCE: 511582001612
CURRENT FILING DATE: 2004-01-05
PRIOR APPLICATION NUMBER: US 09/455,486
PRIOR APPLICATION NUMBER: US 09/455,486
PRIOR FILING DATE: 1999-12-06
PRIOR FILING DATE: 1999-06-01
PRIOR FILING DATE: 1999-06-01
PRIOR FILING DATE: 1998-06-01
PRIOR FILING DATE: 1998-06-01
PRIOR FILING DATE: 1998-06-01
PRIOR FILING DATE: 1998-06-30
NUMBER OF SEQ ID NOS: 47
SOFTWARE: FASTSEQ for Windows Version 4.0
LENGTH: 1193
TYPE: DNA
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Pred. No.:
                                                Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (64)...(1083)
US-10-752-421-1
            US-10-750-262-2
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; Sequence 1, Application US/10752421
; Publication No. US20050063975A1
; GENERAL INFORMATION:
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Application US/10861662
No. US20050086707A1
                                                                               ArgHisGlyTrpGluAspValThrLysIleAsnLysThrGluIleCysSerGlnLeu 339
                                                                  AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG
                                                                                                                      GTCCTGATATTTAAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT
                                                                                                                                      LysGlnPheValTrpTyrThrProProThrPheMetIleAlaValPheLeuProIleVal
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FILE REFERENCE: 51158-20016.26
CURRENT APPLICATION NUMBER: US/10/861,662
CURRENT FILING DATE: 2004-06-04
PRIOR APPLICATION NUMBER: 09/323,873
PRIOR PELLING DATE: 1999-06-01
PRIOR PELLING DATE: 10901-0667
PRIOR PELLING DATE: 2001-12-06
PRIOR APPLICATION NUMBER: 10/011,095
PRIOR APPLICATION NUMBER: 10/211,095
PRIOR FILING DATE: 2001-12-06
PRIOR FILING DATE: 2002-09-06
PRIOR PELLING DATE: 2002-09-06
PRIOR PELLING DATE: 1999-12-06
PRIOR APPLICATION NUMBER: 10/236,486
PRIOR APPLICATION NUMBER: 09/455,486
PRIOR APPLICATION NUMBER: 09/455,486
PRIOR APPLICATION NUMBER: 09/45,486
PRIOR APPLICATION NUMBER: 09/61,183
PRIOR APPLICATION NUMBER: 60/091,183
PRIOR APPLICATION DATE: 1999-12-06
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; LOCATION: (66)...(1085)
US-10-861-662-2
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APPLICANT: Jakobovits, A
APPLICANT: Etessami, Sc
APPLICANT: Challita-Eic
APPLICANT: Perez-Villan
APPLICANT: Perez-Villan
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DB:
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TITLE OF INVENTION: Antibodies and Molecules Derived
TITLE OF INVENTION: therefrom that Bind to STEAP-1
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Jia, Xiao-Chi
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Challita-Eid, Pia N
Perez-Villar, Juan
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Gudas, Jean
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ValSerIleThrLeuLeuAlaLeuValTyrLeuProGlyValIleAlaAlaIleValGln
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FILE REFERENCE: 210121.427C23
CURRENT APPLICATION NUMBER: US/09/759,143
CURRENT FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 934
SOFTWARE: FastSEQ for Windows Version 3.1
SEQ ID NO 878
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APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHO
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE
FILE REFERENCE: 210121.427C23
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Retter, Marc W.
Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
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  ; LENGTH: 1195
; TYPE: DNA
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RESULT 12
US-09-822-827-878
               ; TYPE: DNA
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US-09-822-827-878
Alignment Scores:
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APPLICANT: KU, Jiangchun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: COMPOSITIONS OF PROSTATE CANCER
FILE REFERENCE: 210121.534C1
CURRENT APPLICATION UNMERER: US/09/822,827
CURRENT PILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 982
SOFTWARE: FRASESEQ for Windows Version 3.0
SEQ ID NO 878
LENGTH: 1195
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; ORGANISM: Homo sapiens
US-09-895-793-878
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.534C2
CURRENT APPLICATION NUMBER: US/09/895,793
CURRENT FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 982
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 878
SEQ ID NO 878
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Publication No. US20020192763A1
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Carter, Darrick
Li, Samuel X.
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Kalos, Michael D.
Retter, Marc W.
Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
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Houghton, Raymond L.
Vinals de Bassols, Cárlota
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Hepler, William T.
Henderson, Robert A.
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Publication No. US20020193296A1
GENERAL INFORMATION:
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APPLICANT: Xi, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
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                                      Wang, Aijun
Skeiky, Yasir A.W.
Hepler, William T.
Henderson, Robert A.
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Vedvick, Thomas S.
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Kalos, Michael D.
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McNeill, Patricia
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Houghton, Raymond
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APPLICANT: Vinals de Bassols, Carlota
APPLICANT: POY, Teresa
APPLICANT: FOY, Teresa
APPLICANT: GATYR.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C26
CURRENT APPLICATION NUMBER: US/09/895,814
CURRENT FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 990
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 878
LENGTH: 1195
TYPE: DNA
ORGANISM: Homo sapiens
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; TYPE: DNA
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                                        Percent Similarity:
Best Local Similarity:
Query Match:
US-10-750-262-2 (1-339) x US-10-012-896-878 (1-1195)
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APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT: Wantanabe, Yoshihiro
APPLICANT: Meagher, Madeleine Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C27
CURRENT APPLICATION NUMBER: US/10/012,896
CURRENT FILING DATE: 2001-12-10
NUMBER OF SEC 17 NOC. 1011
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APPLICANT:
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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
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SOFTWARE: FastSEQ for Windows Version 3.0
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Vedvick, Thomas S.
Carter, Darrick
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Kalos, Michael D.
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Houghton, Raymond L.
Vinals de Bassols, Carlota
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Hepler, William T.
Henderson, Robert A.
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Stolk, John A.
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equence 17, App equence 677, Ap equence 60435, equence 193, Ap	215 215 307	equence 77, Applequence 221, Applequence 221, Applequence 3708, Applequence 3708, Applequence 3902, Applequence 401, Applequence 51, Applequence 44589,	quence 40 quence 27 quence 26 quence 41 quence 35 quence 77	equence 4965, A equence 36689, equence 37763, equence 2205, A equence 237, Ap equence 26344, equence 26829, A	, App 225, 209, 381,

ALIGNMENTS

US-10-793-626-3842

i Sequence 3842, Application US/10793626

i Publication No. US2005025478A1

i GENERAL INFORMATION:

i APPLICANT: KIMMERLY, WILLIAM JOHN

i TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS

i FILE REFERENCE: PU3480US

i CURRENT APPLICATION NUMBER: US/10/793,626

CURRENT APPLICATION NUMBER: US/10/793,626

CURRENT FILING DATE: 1999-11-09

NUMBER OF SEQ ID NOS: 4472

SEQ ID NO 3842

I LENGTH: 3137

I TYPE: DNA

ORGANISM: Artificial Sequence
FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: synthetic

OTHER INFORMATION: nucleic acid sequence

US-10-793-626-3842

Alignment Scores:

Pred. No:

OTHER INFORMATION: nucleic acid sequence: 55

Best Local Similarity: 44.07%
Best Local Similarity: 23.70%
Cuery Match: 5.98%

OUESTO Matches: 55

OUESTO Match: 5.98%
COURS MATCHES: 58

DB:

US-10-750-262-2 (1-339) x US-10-793-626-3842 (1-3137)

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                                                            Sequence 48126, Application US/10750185

Publication No. US20050260603A1

GENERAL INFORMATION

APPLICANT: MMI GENOMICS, INC.

APPLICANT: MMI GENOMICS, INC.

APPLICANT: EANISE, Sue K.

APPLICANT: KERR, Richard

APPLICANT: ROSENFELD, David

APPLICANT: BATES, Stephen

APPLICANT: BATES, Stephen

APPLICANT: BATES, Stephen

APPLICANT: PANTIN, Dennis
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                                                                                                                                                                                                                                                     RESULT 2
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING
FILE REFERENCE: MMILLOO-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
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PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIN version 3.1
SEQ ID NO 48126
LENGTH: 2622
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Sequence 3595, Application US/10793626
Publication No. US20050255478A1
GENERAL INFORMATION:
APPLICANT: KIMMERLY, WILLIAM JOHN
APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND
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FILE REPERENCE: PU3480US
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT FILING DATE: 2004-03-04
PRIOR APPLICATION NUMBER: 60/64,258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: Pateentin Ver. 2.1
SEQ ID NO 3595
LENGTH: 3263
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
FEATURE:
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Query Match:
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GTTGCAGCCGTTATTGCGTTTATATAAGTATACGAATTTTCATTTTGAAACAAGCGAGTA 925
                                                            TCACAACGTGTTTTTACTTGGATTTCACTCATAGTATTTTTAGTGATTTCTTATATTGGT 985
                                                                                            Gly-----IleValSerLeuLeuGlyThrIleHis 268
                                                                                                                                                                                        TTTTACATT-----CATTTGTGTCATTGCTGTTGTTTTCCATTTTGCT
                               ---AlaLeuIlePheAlaTrp-----
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154 L 346 -	134 V 286 C	0-750-262-2	ignment Scores: ad. No.: cre: crent Similarity: st Local Similarity ary Match:	ID NO I SUGTH: 1 SUGTH: 1 SUGTH: 1 DAN ISM: 2GANISM: 2ATURE: 2ATURE: 2ATURE: 1 DCATION: 110-977	CORRENT FILE PRIOR APPLI PRIOR APPLI PRIOR APPLI PRIOR FILIN RIOR FILIN RUMBER OF S	FILE OF INVENTION: Composi FILE REFERENCE: CECH118764 CURRENT APPLICATION NUMBER:	110-97 ence 1 icatic RAL IN LICANT LICANT LICANT LICANT		256	236 1087	1027	976	208	916	186	
euAspLysTr	ValileAlaAla :::::: GTGTTGAGTAAA	(1-339) x	••	mo Sap S S ATION:		RENCE: CECH1	Application U Application U S2005026 US2005026 Charmley, Pat Smith, Ryan Argonza-Barr Fitzgibbon, Wang, Kai P.	TTGATAGGT	LysLeuGly:	ThrSerIlePro ::: GAATATGTTACT	AATGCCGGT.	CACGTCGAA	TrpIleGluHisAspVal	TTTATGTGG	ATAATGATG	ValLeuHis
pMetLeuThrAz	.aIleValGlnLe ;;: ACAGACCAAGTT	US-11-110-	5.26 90.50 39.91% 18.42% 5.06%	iens	ν ως ως σ	• •	tion US/11110977 0050260682A1 y, Patrick R. y, Patrick R. Ryan C. Ryan C. Ryan C. Rodora	TTGATAGGTTTAATTÄGTCTTATCATT	LysLeuGlyIleValSerLeuLeuLeu	ProSerValSer	ATTGGCGTTGGC	GGAĠATACAAGC	HisAspVal	LysLeuLeuAsn ::: AATTTAATGCAG	ATAATTCTTAAC	AlaIleTyrSerL
pLysTrpMetLeuThrArgLysGlnPheGlyLeuLeuSerPhePheAlaVal AACCTTCTTTTATTATTGGTCTTTTT	VallleAlaAlaIleValGInLeuHisAsnGlyThrLysTyrLysLysPheProHisTrp ::::: 	977-1 (1-1564)	Length: Matches: Conservative Mismatches: Indels: Gaps:		.12,645 80,514	us/11/110,977	77	ATCATT 1137	LeuLeu 264	ThrSerIleProSerValSerAspSerLeuThrTrpArgGluPheHi ::: GAATATGTTACT	AATGCCGGTATTGGCGTTGGCGGAATCGTAGGTGGACTCGTTATGACACATTTATCAGTG	CACGTCGAAGGAGATACAAGCCAAGTGATGAGTTGGAATATCTCG		TTTATGTGGAATTTAATGCAGTGGAGTACAAATCCAGCTATTCAAAGTGGTATTATTGAA	ATAATGATGATAATTCTTAACTTATTACCAGGAACAGGATTATTATTAGTTGGCTTA	ValLeuHisAlaIleTyrSerLeuSerTyrPro
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GlyLeuLeuSerPhePhePheAlaVal ACCTTCTTTTTATTATTGGTCTTTG	YslysPheProH :::: \GGTCATGCCCTC		64			Diagnosing or Tr				1 00	eredalaredre: 	GTCG	rpArgMetGluIleTyrVals	nGlnAsnLysGl ::: TCAAAGTGGTAT	ATTATTATTAGT	MetAr
						Treating				TyrIleGlnSer ATACTAGTGCA	TCAGTG	-AGTCTC	lSerLeu	uAspAla TATTGAA	TGGCTTA	-MetArgArgSer :::
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR FILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SOPTWARE: SegWin99, version 1.04
SEQ ID NO 2439
LENGTH: 1515
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                                                                                                                                                                                                                              ; TYPE: DNA
; ORGANISM: Neisseria
US-10-467-657-2439
US-10-750-262-2 (1-339) x US-10-467-657-2439 (1-1515)
                                                                                                                                                                                 Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: CHIRON SPA
APPLICANT: FONTANA MARIA RITA
APPLICANT: PIZZA MARIAGRAZIA
APPLICANT: MASIGNANI Vega
APPLICANT: MONACI Elisabetta
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND
FILE REFERENCE:
                                                                                                                                                                No.:
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Gaps: 1-339 x US-11-102-978-3 (1-340000) 57 Cyspro-SerGluLeuGlnHisThrGlnGluLeuPhePro	; PERTURE: ; NAME/KEY: exon ; LOCATION: (216833) ; OTHER INFORMATION: C21orf34 exon US-11-102-978-3 Alignment Scores: Pred. No.: 87.50 Score: 87.54 Percent Similarity: 37.548 Best Local Similarity: 37.548 Best Local Similarity: 22.928 Query Match: 4.898 Indels: 102	FEATURE: NAME/KEY: exon LOCATION: (56948)(57115) COTHER INFORMATION: C21orf34 exon FEATURE: NAME/KEY: misc feature LOCATION: (80006)(81089) COTHER INFORMATION: Gene VDAC2P; voltage-dependent anion channel isoform 2 pseudogene FEATURE: NAME/KEY: exon LOCATION: (167308)(167438) COTHER INFORMATION: C21orf34 exon	NVENTI PLICAT LING I ICATIC ICATIC NG DAI ICATIC NG DAI ICATIC Patent Patent	Db 1212 ACTCCCCAAAGGATGGAACAGTC 1236 RESULT49 1-10-2-978-3 ; Sequence 3, Application US/11102978 ; Publication No. US20050250142A1 ; GENERAL INFORMATION: University of Utah Research Foundation Office APPLICANT: University of Utah Research Foundation
APPLICANT: KIMMERLY, WILLIAM JOHN TITLE OF INVENTION: STARHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS FILE REFERENCE: PUJ480US CURRENT APPLICATION NUMBER: US/10/793,626 CURRENT FILING DATE: 2004-03-04 PRIOR APPLICATION NUMBER: 60/164,258 PRIOR FILING DATE: 1999-11-09 NUMBER OF SEQ ID NOS: 4472 SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 4225 LENGTH: 3083 TYPE: DNA CORANISM: Artificial Sequence FEATURE: OTHER INFORMATION: Description of Artificial Sequence US-10-793-626-4225 Alignment Scores: Pred. No.: Pred. No.: Pred. No.: SOFTWARE: 37.9 SCORE: 87.00 Petcent Similarity: 37.9 SCORE: 97.00 Petcent Similarity: 32.58% Conservative: 35 Best Local Similarity: 22.66% Mismatches: 103 Ouery Match: 135	184 184 184 SULT 10		Db 184355 TAGTGTTGGCTCTGTACCCTCTCGTTTCCCAGTCTATAATCTCTG 184399 Qy 193 UASBTTPALATYTGLIGINVALGINGLASDLASDLASDLASTPILEGLUHISASDVA 213 Db 184400 CTAATGGGGATATCAAAAACCTAGTCACTAAATCAAAGAGCAGTCTGTCCCAGGATGT 184457 Qy 213 1TEPATGMECGIUILETYTVALSETLE 222	149 184235 162 184295

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Indels:	Conservative: 37.09% Conservative: Local Similarity: 22.19% Mismatches:	nt Scores: 9,9	; ORGANISM: Neisseria gonorrhoeae US-10-467-657-4965	; SEQ 1D NO 4965 ; LENGTH: 1068 ; TYPE: DNA	; NUMBER OF SEQ ID NOS: 9218 ; SOFTWARE: SegWin99, version 1.04	; CURRENT FILING DATE: 2001-02-12 ; PRIOR APPLICATION NUMBER: GB-0103424.8 ; PRIOR FILING DATE: 2001-02-12	CAL PROTEINS	MASIGNANI Vega MONACI Elisabetta		; Sequence 4965, Application US/10467657 ; Publication No. US20050260581A1 ; GENERAL INFORMATION:	G.	٠	292 etIleAlaValPhe	591 TGCAATTGTAGGTTAGGTATTAAACTTGTTATAATGGTAC	272	Db 651 TGCAGCAACTTGGTTTGTTAGAATTAAATTATTCTAGGACTTTGTTTG	711 CTTAGGCCAATTTATTGTTATGTTCCTTGGTĞGAATGATAGGTGTCATCTTGATGAGATT	256		220			TTTCGA	Qy 194 nTrpAlaTyrGlnGlnValGlnGlnAsnLysGluAspAlaTrpIleGluHis 211	987 GATTCAAGCAGCAGGTGCTGTTTACTTTAATCTATATGTCTATTAAAAATTTATGGCA	182	Qy 168 rPhePheAlaValLeuHiBAlaIleTyrSerLeuSer	Db 1098 ACATCTACCACCTAAACAACGTAAAAAAGCACTTTTTTATGGCCTATTAGG 1048

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RESULT 14
US-10-750-185-36689
; Sequence 36689, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
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                                                                                                                                    HisGly 323
                                                                                                                                                                                                                                    CGTATCGGCCTGTCGCCGTTTTGGGTTATCTTTTCGCTGATCGCGTTCGGAGAGCTGATG
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APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMIL1100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
PRIOR FILING DATE: 2002-12-31
VUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIN version 3.1
SEQ ID NO 36689
LENGTH: 1138
TYPE: DNA
ORGANISM: Bovine 19866880906331
US-10-750-185-36689
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                139 CTTAATTGAATGTACTTTCACTTTGCAATAATTAGCCCTTCACATATTCCAGTAAACTTA 198
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ROSENFELD, David
HOLM, Tom
BATES, Stephen
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                                                                                                                                                                                                                                                                 CAAGATÖGTAATAATCTTATCTATAATGAGTTTCTCTÄTAGGAGATTCACTGGCATAGAG 447
                                                                                                                                                                                                                                                                                            HisAsnGlyThrLys-------TyrLysLysPhe-----
                                                                                                                                                                                                                                                                                                                                SerIleThrLeuLeuAlaLeuValTyrLeuProGlyValIleAlaAlaIleValGlnLeu 141
                                                                                                                                                                                                                                                                                                                                                                                                                               pheTyrLysIleProIleLeuValIle-----AspLysValLeuProMetVal 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTCATCAAGACTCTTGTG------TTTATAGATGCA
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                                                                                                                                                               LeuSerPhePhePheAlaValLeuHisAlaIleTyrSerLeuSerTyrProMetArgArg 186
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|-----TTTTGGTTTTGTTTTGTTCTTTCTATATTCTCCTGAGTTCTAACATATCACGCT 525
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                                                                                                                                                                                                                              TCAGTAAGATATAAAATATATGCATAGCTGGTAGAAAGACACTTTCAAGATACAGTTTCA 585
                                                                                       SerTyrArgTyrLysLeu-Leu---AsnTrp------
               --AlaTyrGlnGlnValGlnGlnAsnLysGluAspAlaTrpIleGluHisAs 212 | | | | | | | | | ::: :: :::
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OV 212 PRAITPACHMEGIUITTYVACCAMGEMATAGTITTMACCAMGEMAGGG 645 OV 212 ULBALAVAITPACHMEGIUITTYVALSETLEUGYILEVALGILEUALALE 212 Db 766 CANTOGOTGOTGOTGOTTATTAGGATGGAMATAGTTTTTMACCAMGG 645 OV 214 LABALAVAITHASETLEVAGGGCACTACACTAGTGGGAMATAGTGTTTTTMACCAGGG OV 214 LAGGLUBBELGTTGTTTTAGGCCCCCAACTAGTGGTGCTAACTAGTGCTTTTAGGCCTCAACTAGTGGTGCTTACCTGAGGC 76 OV 216 LAGGLUBBELGTTTTTAGGCCCCCAACTAGTGCTCAACTAGTCTGCTTAACTAGGCCTCAACTAGTGCTTTAACTCTGAAAA 86 OV 227 ETCOFTOTTTAGGCCCCCCAACTAGTCCCAACTAGTCTGCTTAAAATCTGCCTCAAAATTTTAAAACTGCCTCAAAATTTTAGGCCTCCAACTAGTCTGCTAAAATTTGCAACAAAATTTTAAAACTGCCTCAAAATTTTAAAACTGCCTCAAAATTTTAAAATTTGCAACAAAATTTTAAAACTGCCTCAAAATTTAGGCCTCCAAAATTTTAAAATTTGCAACAAAATTTCAAAATTTGCAACAAAATTTTAAAATTCACTTTAAAAATCGCCTCAAAAATTTAGGCAACAAAATTTAGGCAACAAAATTTAGGCAACAAAATTTAGGCAACAAAATTTAGGCAACAAAATTTAGGCAACAAAATTTAGGCAACAAAATTTAGGCAACAAAATTTAGGCAACAAAATTTAGGCAACAAAATTTAGGCAACAAAATTTAGGCAACAAAAAAAA
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Search completed: December 6 2005 18.50.55	Search
928 GAIGICITICCTCTTCATCATCATGTCTCTTCCATCCTATTAATAGCTTGG 871	D _D
258 yIleValSerLeuLeuGlyThrIleHisAlaLeuIlePheAlaTrp 274	8
982 CCCCAGCTCAAAGGATCTCAGCACAGAGGCCCATAAAAGAGCCCATGAAAATCGT 929	da
239 -ProSerValSerAspSerLeuThrTrpArgGluPheHisTyrIleGlnSerLysLeuGl 258	Ş
1042 GACCTCACTGCTCCTCTTAGTTCTCTCCTTGATGAGACACATCAGGAATTTTGCAGTTCAA 983	Ъ
235 ThrSerIle 238	Ş
1090 GTTGATTGTTTTTAACTTCATCAACTTAATCCCCTTTCTTCTGTCCCT 104	Ф
215 gMetGluIleTyrValSerLeuGlyIleValGlyLeuAlaIleLeuAlaLeuLeuAlaVa 235	γQ
1126 GTCCTCAGATGTAAGTGAAACTCATTATCTTCACCA 109	뭣
195 pAlaTyrGlnGlnValGlnGlnAsnLysGluAspAlaTrpIleGluHisAspValTrpAr 215	Ş
1186 ATATACACTTAGTCATATCTTAACTAACAGCTACAAAATATATGTAAGAAACTCAACGTG 112	DЬ
177 eTyrSerLeuSerTyrProMetArgArgSerTyrArgTyrLysLeuLeuAsnTr 195	Ş
1246 TGTGGTACTGGTGCTTCTCTTGGGGTCTTTGTCCTTACTGTTTTTGAATTATGAATCAAT 118	뭥
164PheGlyLeuLeuSerPhePhePheAlaValLeuHisAlaIl 177	ş

Search completed: December 6, 2005, 18:50:55 Job time : 320 secs

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Result
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-MODEL-frame+ p2n.model -DEV=xlh
-Q=/cgn2 1/USPTO_spool h/US10750262/runat 06122005 162946 15642/app query.fasta_1.519
-D=Issued_Patents_NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCI=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCOREspot -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10750262 @CGN 1 1 193 @runat 06122005 162946 15642 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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1: /cgn2_6/ptodata/1/ina/1_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
7: /cgn2_6/ptodata/1/ina/PE_COMB.seq:*
9: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-759-143-878

US-09-759-143-878

US-10-010-667A-1

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	Sequence 4, Appli Sequence 6, Appli Sequence 342, App Sequence 5, Appli Sequence 10, Appli Sequence 1185, App Sequence 1185, App Sequence 1185, App Sequence 3, Appli Sequence 3, Appli Sequence 6, Appli Sequence 7, Appli Sequence 7, Appli Sequence 7, Appli Sequence 33, Appli Sequence 215, App	

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Percent Similarity:
Best Local Similarity:
                                                             Pred. No.:
                                                                                  Alignment Scores:
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GENERAL INFORMATION:

APPLICANT: Daniel E. Afar

APPLICANT: Rene S. Hubert

APPLICANT: Arbur B. Raitano

APPLICANT: Douglas C. Saffran

APPLICANT: Stephen C. Mitchell

TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS

TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF

FILE REFERENCE: 129.17-US-11

CURRENT APPLICATION NUMBER: US/09/455,486

CURRENT FILING DATE: 1399-12-06

DETICE ADDITION NUMBER: 09/323.873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application Patent No. 6833438 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 09/PRIOR FILING DATE: 1999-06-01
                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                            TYPE: DNA
                                                                                                                                                                                  ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                               NAME/KEY: CDS
                                                                                                                                              LOCATION:
                                                                                                                                                                                                                                                                                     FastSEQ for Windows Version 4.0
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Matches:
Conservative:
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APPLICANT: Rene S. Hubert
APPLICANT: Kahan Leong
APPLICANT: Arthur B. Raitano
APPLICANT: Arthur B. Raitano
APPLICANT: Douglas C. Saffran
APPLICANT: Steve Chappell Mitchell
APPLICANTON: EXPRESSED IN HUMAN CANCERS AND USES THEREO
TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREO
TILLE REFERENCE: 129.16USU2
CURRENT APPLICATION NUMBER: US/09/323,873A
CURRENT FILLING DATE: 1999-06-01
PRIOR APPLICATION NUMBER: 60/087,520
PRIOR APPLICATION NUMBER: 60/091,183
PRIOR APPLICATION NUMBER: 60/091,183
PRIOR FILLING DATE: 1998-06-30
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSEQ for Windows Version 4.0
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APPLICANT: W. Jiangchun

APPLICANT: Mitcham, Jennifer L.

APPLICANT: Harlocker, Susan L.

APPLICANT: Harlocker, Susan L.

APPLICANT: Harlocker, Susan L.

APPLICANT: Henderson, Notherland

APPLICANT: Henderson, Notherland

APPLICANT: Kalos, Michael D.

APPLICANT: Kalos, Michael D.

APPLICANT: Retter, Marc W.

APPLICANT: Body Craig H.

APPLICANT: Day, Craig H.

APPLICANT: Vedvick, Thomas S.

APPLICANT: Li, Samuel

APPLICANT: Li, Samuel

APPLICANT: Wang, Aijun

APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Wang, Aijun

APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Hepler, William

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

CURRENT APPLICATION NUMBER: US/09/685,166A

CURRENT FILING DATE: 2000-10-10
                                                                                          NUMBER OF SEQ ID NOS: 898
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 878
LENGTH: 1195
TYPE: DNA
ORGANISM: Homo sapiens
US-09-685-166A-878
Percent Similarity:
Best Local Similarity:
                                                  Alignment Scores: Pred. No.:
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US-09-685-166A-878
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APPLICANT: Skekky, Yasir A.W.
APPLICANT: Hepler, William
FITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
FITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C20
CURRENT APPLICATION NUMBER: US/09/679,426
CURRENT FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 895
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 878
LENGTH: 1195
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Best Local Similarity:
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; Sequence 878, Application US/09679426
; Patent No. 6759515
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Retter, Marc W.
Stolk, John A.
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Vedvick, Thomas S.
Carter, Darrick
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Kalos, Michael D.
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Dillon, Davin C.
Mitcham, Jennifer L.
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Patent No. 6800746
GENERAL INFORMATION:
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                                         FILE REFERENCE: 210121.437C23
CURRENT APPLICATION NUMBER: US/09/759,143
CURRENT FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 934
SOFTWARE: FastSEQ for Windows Version 3.1
                                                                               APPLICANT: Skelky, Yasir A.W. APPLICANT: Hepler, William TITLE OF INVENTION: COMPOSITIONS TITLE OF INVENTION: DIAGNOSIS OF FILE REFERENCE: 200121.427023
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LENGTH: 1195
TYPE: DNA
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Vedvick, Thomas (
Carter, Darrick
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Henderson, Robe
Kalos, Michael
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Mitcham, Jennifer L.
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ORGANISM: Homo
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APPLICANT: RAITANO, Arthur B.
APPLICANT: Saffran, Douglas C.
APPLICANT: Mitchell, Steve Chappell
TITLB OF INVENTION: NOVEL SERPENTINE TRANSNEMBRANE ANTIGENS
TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREO
FILE REFERENCE: 511582001601
CURRENT APPLICATION UNMBER: US/10/010,667A
CURRENT FILING DATE: 2001-12-06
PRIOR APPLICATION NUMBER: 09/323,873
PRIOR FILING DATE: 1999-06-01
PRIOR APPLICATION NUMBER: 60/087,520
PRIOR APPLICATION NUMBER: 60/087,520
PRIOR APPLICATION NUMBER: 60/091,183
PRIOR FILING DATE: 1998-06-01
PRIOR PILING DATE: 1998-06-30
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSEQ for Windows Version 4.0
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Query Match:
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APPLICANT: AKar, Daniel
APPLICANT: Hubert, Rene S
APPLICANT: Leong, Kahan
APPLICANT: Raitano, Archu
APPLICANT: Saftan, Dougl
APPLICANT: Mitchell, Stev
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APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Yiang, Yuqiu
APPLICANT: Kalos, Michael D.
APPLICANT: Kalos, Michael D.
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
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          ANT: Foy, Teresa
ANT: Fanger, Gary R.
ANT: Wantanabe, Yoshihiro
ANT: Meagher, Madeleine Joy
FINVENTION: COMPOSITIONS AND
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Skeiky, Yasir A.W.
Hepler, William T.
                                                                                                                                                                    Day, Craig H.
Vedvick, Thomas S
Carter, Darrick
                                                                  McNeill, Patricia D.
Houghton, Raymond L.
Vinals de Bassols, Carlota
                                                                                                                 Henderson, Robert A
                                                                                                                                                            Li, Samuel X.
                                                                                                       John
  COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS OF PROSTATE CANCER
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Percent Similarity:
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Query Match:
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CURRENT APPLICATION NUMBER: US/10/012,896
CURRENT FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 1011
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 878
LENGTH: 1195
TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                            <u>ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT</u>
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                                                                                                        | GlnGlnAsnLysGluAspAlaTrpIleGluHisAspValTrpArgMetGluIleTyrVal
                                                                                                                                       TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC
                                                                                                                                                                                   ValSerAspSerLeuThrTrpArgGluPheHisTyrIleGlnSerLysLeuGlyIleVal
                                              TCTCTGGGAATTGTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT
                                                          SerLeuGlyIleValGlyLeuAlaIleLeuAlaLeuLeuAlaValThrSerIleProSer 240
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; SOFTWARE: FastSEQ for Windows Version
; SEQ ID NO 2686
; LENGTH: 1147
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-2686
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US-09-949-016-2686
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2686, Ap
Patent No. 681233
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SerHi8GlnGlnTyrPheTyrLy8IleProIleLeuVallleAsnLy8ValLeuProMet 120
                                                       IleAlaSerLeuThrPheLeuTyrThrLeuLeuArgGluValIleHisProLeuAlaThr
                                                                                             ĊTTCAGCACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT
                                                                                                               LeuGlnHisThrGlnGluLeuPheProGlnTrpHisLeuProIleLysIleAlaAlaIle
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                                                                                                                                                                  ProValLeuLeuHisGenThrAlaHisAlaAspGluPheAspCysProSerGlu
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           LENGTH: 3627
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GENERAL INFORMATION:

GENERAL INFORMATION:

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APPLICANT: Douglas C. Saffran

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TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREO

FILE REFERENCE: 129.16USU2

CURRENT APPLICATION NUMBER: US/09/323,873A

CURRENT FILING DATE: 1999-06-01

PRIOR APPLICATION NUMBER: 60/091,520

PRIOR APPLICATION NUMBER: 60/091,183

PRIOR APPLICATION NUMBER: 60/091,183

PRIOR FILING DATE: 1998-06-30

NUMBER OF SEQ ID NOS: 32

SOFTWARE: FastSEQ for Windows Version 4.0

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2015 CAACATTCTCACAGAATTTCCTAATTTTGTAGGTTCAGCCTGATAACCACTGGAGTTCTT	N
253	Db 875 TAACCCTAAGAGGTAAATCTTCTTTTTGTGTTTATGATATAGAATATGTTGACTTTACCC 934 Qy
1955 CTGATTAGTTTGGAAAGTATGCCTCCATCTGAATTAGTCCAGTGTGGCTTAGAGTTGGTA 2014	Qy 253 253 pb
1895 GACATTCGCAACTATCCCTTCTACATGTCCACACGTATACACGTATACTCCACACGTATACTCCACACGTATACTCCACACGTATACTCCACACGTATACTCCACACGTATACTCCACACGTATACTCCACACGTATACTCCACACGTATACTCCACACGTATACTCCACACGTATACTCCACACGTATACTCCACACGTATACTCCACACGTATACTCCACACGTATACTCCACACGTATACTCCACACGTATACTCCACACGTATACTCCACACGTATACTCCACACGTATACACACGTATACACGTATACACGTATACACACGTATACACGTATACACACGTATACACACGTATACACACGTATACACACGTATACACACGTATACACACGTATACACACAC	
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1835 TCATGAACACTGCCAATTACCGTTTATGGGTAGACATCTTTGGAAATTTCCACAAGGTCA 1894	21 SerLeuGlyIleValGlyLeuAlaIleLeuAlaLeuLeuAlaValThrSerIleProSer 2
253	696 CAACAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTTGGAGAATTGGAGATTTATGTG 755
1775 GTGCCAGAATCACTCTGGGATCCTTGTCTGACAAGATTCAAAGGACTAAATTTAATTCAG	SlnAsnLysGluAspAlaTrpIleGluHisAspValTrpArgMetGluIleTyrVal 220
1715 ACTATCTCAGATTTACTGAGGTTTATCTTCTGGTGGTAGATTATCCATAANAANAANAA	QY 181 SerTyrProMetArgArgSerTyrArgTyrLyBLetLetChant. Philippe Communication of the Communicat
253	6 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCA
1655 CCAGCTTACATTTTATATACTTACTCACTTGAAGTTTCTAAATATTCTTGTAATTTTAAA	98GlnPheGlyLeuLeuSerPhePhePheAlaValLeuHisAlaIleTyrSerLeu 18
	516 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGG
253TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	41 LeuHisAsnGlyThrLysTyrLysLysPheProHisTrpLeuAspLysTrpMetLeuThr 160
1535 AGTAATGCCTTTTATGTTACACAACTTAGCACTTTCCAGAAACACAAAACTCTCTCCTTGA	121 valSerIleThrLeuLeuNalAleuValTyrLeuProGLyValIleAlaAlaiLeValGin 140
253	TCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 45
1475 CCAATATGCATGGTTTATTATTTCTTAAAAAAAATATTCTTTTACCTGTCACCTGAATTT	erHisGlnGlnTyrPheTyrLysIleProIleLeuVallleAsnLysValLeuProMet 120
253	CTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCCTTAGCAACT 3
1415 TTCTAATATTTGAAACTTGTTAGACAATTTGCTACCCATCTAATGTGATATTTTAGGAAT	aSerLeuThrPheLeuTyrThrLeuLeuArgGluVallleHisProLeuAlaThr 100
253	TCAGCACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 335
1355 CACCTCGGCCTCCCAAAGTGCTGGGATGACAGTTGTGAGCCACCACACTCAGCCTGCTCT	rrGlnGluLeuPheProGlnTrpHisLeuProIleLy8IleAlaAlaIle 80
253	GTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT
1295 GACAGGGTTTTCCCATGTTGGCCAGGCTGGTCTCGATCTCCTGACCTCAAATGATCCGCC	41 ProValLeuLeuHisCeuHisCanThrAlaHisAlaAspGluPheAspCysP
	156 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAAGA 215
1235 AGTAGCTGGGATTACAGGCACCCATCACCATGTCCAGCTAATTTTTGTATTTTAGTAGA	sAspThrGlyGluThrSerMetLeuLysArg 40
	96 ATGGAAAGCAGAAAAAGACATCACAAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 155
1175 CTCGGCTCACTGCAACCTGCGCCTCCTGGGTTCAGGCGATTCTCTTGCCTCAGCCTCCTG	spileThrAsnGlnGluGluLeuTrpLysMetLysProArgArg 20
253	US-10-750-262-2 (1-339) x US-09-323-873A-6 (1-3627)
1115 GTTTGTTTTTTGAGATGAAGTCTCGCTCTGTTGCCCATGCTGGAGTACAGTGGCACGAT	ry Match: 75.89% indexe: 001
253	t Local Similarity: 29.68% Mismatches:
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QY 81	Db 276 CTTCAGCACACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 335	216 CCTGTCTTTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA	41		v		Maccn: 75.89% Indels: 3.89% Gaps:	Int Similarity: 29.68% Conservative: Local Similarity: 29.68% Mismatches:		gnment Scor		; LENGTH: 3627 ; TYPE: DNA	EQ for	; PRIOR FILING DATE: 1999-06-01; NUMBER OF SEQ ID NOS: 34	CURRENT FILING DATE: 109/433,486 CURRENT FILING DATE: 1099-12-06 PRIOR APPLICATION NUMBER: 09/323,873	TIC /OC /AFF ACC	TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND HERESOF			FORMATI	Sequence 4, Application US/09455486; Patent No. 6833438	RESULT 10 US-09-455-486-4	Db 3455 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 3511	Qy 321 ArgHisGlyTrpGluAspValThrLysIleAspLysThrGluIleCysSerGlnLeu 339	Db 3395 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGAAGAAGATACTGAAGATT 3454	Qy 301 ValLeuIlePheLysSerIleLeuPheLeuProCysLeuArgLysLysIleLeuLysIle 320	Db 3335 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTATTGTT 3394	Qy 281 LysGlnPheValTrpTyrThrProProThrPheMetIleAlaValPheLeuProIleVal 300	Db 3275 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATATATA 3334		Qy 254GlnSerLysLeuGlyIleVal 260

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253	355 CACCTCGGCCTCCCAAAGTGCTGGGATGACAGTTGTGAGCCACCACACTCAGCCTGCTCT 1414 Qy
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253	.295 GACAGGGTTTTCCCATGTTGGCCAGGCTGGTCTCGATCTCCTGACCTCAAATGATCCGCC 1354 Qy
2375 GATTGTATTCACTGGGACTTAAGAATGCGCCTGAATAATTGTGAGTTCGATTTGTTCTGG	
253	.235 AGTAGCTGGGATTACAGGCACCCATCACCATGTCCAGCTAATTTTTGTATTTTTAGTAGA 1294 Qy
2315 ACTGGTTACACTACAAGTTACCTTGGAGATTCATATATGAAAACGCAAACTTAGCTATTT	253
253	.175 CTCGGCTCACTGCAACCTGCGCCTCCTGGGTTCAGGCGATTCTCTTGCCTCAGCCTCCTG 1234 Qy
2255 CAACCAATGACATGTATTTTTCAACTAGTAACCTAGAAATGTTTCACTTAAAATCTGAGA	253 253 Db
253	1115 GTTTGTTTTTTGAGATGAAGTCTCGCTCTGTTGCCCCATGCTGGAGTACAGTGGCACGAT 1174 Qy
2195 TATATGTACAATACCTAGCCCATAATAGGTATACAATACACATTTGGTAAAACTAATTTT	253 253 Db
253	055 TAAAAGGCATTAAAATATTCTTTGTTTTTTTTTTTTTTGTTTTGTTTTTTTT
2135 CTGCTTTTTAGACTTCATTAGGAATTTAGGACTGCATCTTGACAACTGAGCCTATTCTAC	253
253	995 GTGCTCTCCTGTTGTTTTCCCTATTGCTTCTAATTAGGACAAGTGTTTCCTAGACATAAA 1054 Qy
2075 TGGTCCTCATTAAATAGCTTTCTTCACACATTGCTCTGCCTGTTACACATATGATGAACA	253
253	935 CATAAAAAATAACAAATGTTTTTCAACAGCAAAGATCTTATACTTGTTCCAATTAATAAT 994 Qy
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253	875 TAACCCTAAGAGGTAAATCTTCTTTTTGTGTTTATGATATAGAATATGTTGACTTTACCC 934 Qy
1955 CTGATTAGTTTGGAAAGTATGCCTCCATCTGAATTAGTCCAGTGTGGCTTAGAGTTGGTA	
253	8
1895 GACATTCGCAACTATCCCTTCTACATGTCCACACGTATACTCCAACACTTTATTAGGCAT	241 ValSerAspSerLeuThrTrpArgGluPheHisTyrIle 253
253	
1835 TCATGAACACTGCCAATTACCGTTTATGGGTAGACATCTTTGGAAATTTCCACAAGGTCA	221 SerLeuGlyIleValGlyLeuAlaIlcLeuAlaLeuLeuAlaValThrSerIleProSer 240 Db
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1775 GTGCCAGAATCACTCTGGGATCCTTGTCTGACAAGATTCAAAGGACTAAATTTAATTCAG	0
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1715 ACTATCTCAGATTTACTGAGGTTTATCTTCTGGTGGTAGATTATCCATAAGAAGAGTGAT	.81 SerTyrProMetArgArgSerTyrArgTyrLysLeuLeuAsnTrpAlaTyrGlnGlnVal 200 Db
253	576 AGANAGCAGTTTGGGCTTCTTGTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 635
1655 CCAGCTTACATTTTATATACTTACTCACTTGAAGTTTCTAAATATTCTTGTAATTTTAAA	61 ArgLysGlnPheGlyLeuLeuSerPhePhePheAlaValLeuHisAlaIleTyrSerLeu 180
253	516 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGG
1595 AATAATAGAGTTTTTATCTACCAAAGATATGCTAGTGTCTCATTTCAAAGGCTGCTTTTT	141 LeuHisAsnGlyThrLysTyrLysPheProHisTrpLeuAspLysTrpMetLeuThr 160 Db
253	456 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 515
1535 AGTAATGCCTTTTATGTTACACAACTTAGCACTTTCCAGAAACAACAAAACTCTCTCCTTGA	
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1475 CCAATATGCATGGTTTATTATTTCTTAAAAAAAATATTCTTTTACCTGTCACCTGAATTT	120
253	36 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATICACCCCTTAGCAACT

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                          Sequence 6, Application US/10010667A
PATERIX NO. 6887975
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APPLICANT: Afar, Daniel
APPLICANT: Hubert, Rene S.
APPLICANT: Leong, Kahan
APPLICANT: Raitano, Arthur B.
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Query Match:
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 09/323,873
PRIOR FILING DATE: 1999-06-01
PRIOR APPLICATION NUMBER: 60/087,520
PRIOR FILING DATE: 1998-06-01
PRIOR APPLICATION NUMBER: 60/091,183
PRIOR FILING DATE: 1998-06-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Saffran, Douglas C.
APPLICANT: Mitchell, Steve Chappell
TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF
FILE REFERENCE: 511582001601
CURRENT APPLICATION NUMBER: US/10/010,667A
CURRENT FILING DATE: 2001-12-06
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TYPE: DN
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ORGANISM: Homo
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           GlnGlnAsnLysGluAspAlaTrpIleGluHisAspValTrpArgMetGluIleTyrval
                                                                            SerTyrProMetArgArgSerTyrArgTyrLysLeuLeuAsnTrpAlaTyrGlnGlnVal
                                                                                                                                      ArgLysGlnPheGlyLeuLeuSerPhePheAlaValLeuHisAlaIleTyrSerLeu
                                                                                                                                                                              LeuHisAsnGlyThrLysTyrLysLysPheProHisTrpLeuAspLysTrpMetLeuThr
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Db 2795 TCTTCAATCTACCTATATTTAATTGAGAATCTAAAATGTACAAATCATTGTGTTGATTCT 2854 Db 2795 TCTTCAATCTACCTATATTTAATTGAGAATCTAAAATGTACAAATCATTGTGTTGATTCT 2854 Db 2855 GCAGTGATCCTGCTATAAGTAAGACTCAGTCCCTGATTTTAGGTATCCTGTGAAAAGCAG 2914	2675 TTTAAAACATAGGCCAAGTTCALLCALLCALLCALLCALLCALCALCALCALCALCALCA	253 2615 253	Qy 253 Db 2495 TGTCAGAACACCGTTGAGATTACATAGGTGAACAACTATTTTTTAAGCAACTTTATTTGTG 2554 Qy 253 Db 253 TAGTGACAAAGCATCCCAATGCAGGCTGAAATGTTTCATCACATCTCTGGATCTCTCTAT 2614	Db 2375 GATTGTATTCACTGGGACTTAAGAATGCGCCTGAATAATTGTGAGTTCGACTTGTGTGTCTGG 2434 Qy 253		Qy 253 253 Db 2195 TATATGTACAATACCTAGCCCATAATAGGTATACAATACACATTTGGTAAAACTAATTTT 2254 Qy 253 253 Qy 255 CAACCAATGACATGTATTTTCAACTAGTAACCTAGAAATGTTTCACTTAAAATCTGAGA 2314	Qy 253 253 253 2134 2134 2134 2134 2134 2134 2134 2134 2134 2134 2134 2134 2134 2134 2134 2135 2135 2135 2135 2135 2136 2135 2135 2135 2135 2135 2135 2135 2135 2135 2135 2135 2135 2135 2135 2135 2136 2135 2135 2135 2135 2135 2135 2136	

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253 253	6228 ATCACTGAAGTCAAATTGATTTTTGCTATAATCTTCAATCTACCTATATTTAATTGAGAA 6287	253 253	6168 TCATTATTCATTTATCAAAATCAGAGTGAATCACATTAGTCGCCTTCACAACTGATAAAG 6227		6108 ATTATTTCCATGTTATCAGAATATTTGATTTTTTAAAAACATAGGCCAAGTTCATTCA	253 253	6048 AATGTTTCATCACATCTCTGGATCTCTCTATTTTGTGCAGACATTGAAAAAATTGTTCAT 6107		5988 GAACAACTATTTTTAAGCAACTTTATTTGTGTAGTGACAAAGCATCCCAATGCAGGCTGA 6047		5928 ATAGAGGTCAGAAGTCGTATAAAAGAGGTGTTGTCAGAACACCGTTGAGATTACATAGGT 5987		5868 CCTGAATAATTGTGAGTTCGATTTGTTCTGGCAGGCTAATGACCATTTCCAGTAAAGTGA 5927	253 253	5808 TTCATATATGAAAACGCAAACTTAGCTATTTGATTGTATTCACTGGGACTTAAGAATGCG 5867		5748 AACCTAGAAATGTTTCACTTAAAATCTGAGAACTGGTTACACTACAAGTTACCTTGGAGA 5807		5688 TATACAATACACATTTGGTAAAACTAATTTTCAACCAATGACATGTATTTTTCAACTAGT 5747	253 253	5628 GACTGCATCTTGACAACTGAGCCTATTCTACTATATGTACAATACCTAGCCCATAATAGG 5687	253 253	5568 ATTGCTCTGCCTGTTACACATATGATGAACACTGCTTTTTAGACTTCATTAGGAATTTAG 5627	253 253	5508 TAGGITCAGCCTGATAACCACTGGAGTTCTTTGGTCCTCATTAAATAGCTTTCTTCACAC 5567	253 253	5448 TGAATTAGTCCAGTGTGGCTTAGAGTTGGTACAACATTCTCACAGAATTTCCTAATTTTG 5507	253 253	5388 CACACGTATACTCCAACACTTTATTAGGCATCTGATTAGTTTGGAAAGTATGCCTCCATC 5447		5328 GTAGACATCTTTGGAAATTTCCACAAGGTCAGACATTCGCAACTATCCCTTCTACATGTC 5387		5368 GACAAGATTCAAAGGACTAAATTTAATTCAGTCATGAACACTGCCAATTACCGTTTATGG 5327	•

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		of both is positive, were	
Alignment Scores:	_	TYPE: DNA	٠.
; ORGANISM: Homo US-09-352-616A-342		ID NO 342 ENGTH: 592	; SEQ
; LENGTH: 592		NUMBER OF SEQ ID NOS: 575 SOFTWARE: FASTSEQ for Windows Version 3.0	 g z
; SEQ ID NO 342		CURRENT FILING DATE: 1999-11-12	
70		TILE REFERENCE: 210121.427C9	
; CURRENT APPLICA ; CURRENT FILING		AND METHOD	 -
; FILE REFERENCE;	-	APPLICANT: Solk, John APPLICANT: Day, Craig	 > >
; TITLE OF INVENT			··· >
; APPLICANT: Xu,	<u>-</u> -	Kalos	. v.
; APPLICANT: Jia		APPLICANT: Reed, Steven G.	 >>
; APPLICANT: Dil		Harlocker, Susan L	· ·.
; Facent No. 6395; GENERAL INFORMAT		APPLICANT: Dillon, Davin C. APPLICANT: Mitcham. Jennifer T.	 e e
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RESULT 14		Sequence 342, Application US/09439313	
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Оу 21 Авг	_	6528 AGAAATTACCCAAAAGTAAGGTGAGGAGGATAGGCAAAAAGAGTAGAAAGATGTGAATGG 6587	밁
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US-10-750-262-2	_	253 253	S S
Query Match: DB:	_	6408 ACAAAAATATATCATAAGGGGATGAACAAAATGGTGGAGAAAGAGTAGACAAAGTTT 6467	망
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; ORGANISM: Ho	_	6288 TCTAAAATCTACAAATCATTCTTCTTCTTCTTCTTCTCCCCCC	~

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IT: Xu, Jiangchun
TI: Mitcham, Jennifer Lynn
INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE
TERENCE: 210121.427C8
APPLICATION NUMBER: US/09/352,616A
FILING DATE: 1999-07-13
P SEQ ID NOS: 472
P SEQ ID NOS: 472
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342, Application US/09352616A
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                              : FastSEQ for Windows Version 3.0
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Harlocker, Susan Louise
Jiang, Yuqui
Xu, Jiangchun
Xu, Jiangchun
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APPLICANT: XU, Jiangchun
APPLICANT: Mitcham, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Kalos, Michael D.
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Carter, Darrick
APPLICANT: Carter, Darrick
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
APPLICANT: Mang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
APPLICANT: Hepler, William
APPLICANT: Hepler, William
APPLICANT: Brang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Stolk, Yasir A.W.
APPLICANT: Hepler, William
APPLICANT: Hepler, William
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.42717C17
CURRENT APPLICATION NUMBER: US/09/636,215
CURRENT FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 852
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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; SEQ ID NO 342
; LENGTH: 592
; LENGTH: 592
; TYPE: DNA
; ORGANISM: HOMO 8
; ORGANISM: HOMO 8
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                                                                                                                                                                     LeuGlnHisThrGlnGluLeuPheProGlnTrpHisLeuProIleLysIleAlaAlaIle
                                                                                                                                                                                                                                                           CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA
                                                                                                                                                                                                                                                                        ProValLeuLeuHisLeuHisGlnThrAlaHisAlaAspGluPheAspCysProSerGlu
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          ArgLysGlnPheGlyLeuLeuSerPhePhePheAla 172
                                                                                               ValSerIleThrLeuLeuAlaLeuValTyrLeuProGlyVallleAlaAlaIleValGln 140
                                                                                                                                         | SerHi8GlnGlnTyrPheTyrLy8IleProIleLeuVallleAsnLy8ValLeuProMet
                                                                                                                                                                                                                 CTTCAGCACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT
                                                      LeuHisAsnGlyThrLysTyrLysLysPheProHisTrpLeuAspLysTrpMetLeuThr
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Perfect score:
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1: /cgn2_6/ptodata/2/pubpna/US09

2: /cgn2_6/ptodata/2/pubpna/US07

3: /cgn2_6/ptodata/2/pubpna/US07

4: /cgn2_6/ptodata/2/pubpna/US07

4: /cgn2_6/ptodata/2/pubpna/US10

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10: /cgn2_6/ptodata/2/pubpna/US11
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/cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
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US-11-108-172-547
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US-10-750-185-37153
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US-10-750-185-39315
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Sequence 35293, A
Sequence 3, Appli
Sequence 547, App
Sequence 54184, A
Sequence 27, Appl
Sequence 27, Appl
Sequence 64012, A
Sequence 64012, A
Sequence 62619, A
Sequence 3615, A
Sequence 24645, A
Sequence 57153, A
Sequence 57153, A
Sequence 57153, A
Sequence 57153, A
                                                                                                                                                                                                              Sequence 25365, A
Sequence 39315, A
Sequence 49060, A
Sequence 54610, A
Sequence 33875, A
Sequence 30880, A
Sequence 142, App
Sequence 48714, A
Sequence 38532, A
Sequence 35293, A
Sequence 3, Appli
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-48	5-3	6	5-5	1-47	-49	4.	2	-26	44	-14	3-46	-17	-13	-5	35	-38	5-40	5-4	-4	٠ <u>.</u>	
3072	-10-750-185-30138	-10-750-185-63586	-10-750-185-54609	_	_	62	7481	3-10-750-185-26752	1414	85	Ο,	6	75	2241	-10-750-185-39246	US-10-750-185-38045	23	179	US-10-750-185-47856	160	
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ALIGNMENTS

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APPLICANT: MMI GENOMICS, INC.
APPLICANT: MMI GENOMICS, Sue K.
APPLICANT: KERR, Richard
APPLICANT: KERR, Richard
APPLICANT: HOLM, Tom
APPLICANT: HOLM, Tom
APPLICANT: HAVIN, Dennis
ITILE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMI1100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR OF SEQ ID NOS: 64922
SOFTWARE: PATENCE IN SEQ ID NO 25365
LENGTH: 1779
TYPE: DNA
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; ORGANISM: Bovine 19866880604913
US-10-750-185-25365
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US-10-750-185-25365
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Publication No. US20050260603A1
GENERAL INFORMATION:
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Local Similarity 54.1%; Pred. No. 0.1;
tes 80; Conservative 0; Mismatches
885 TAACTTATATTTTAAAAAACAATGTTGT
                                         824 ATAAGTGGATAGATATAAAACAATTTGT 851
                                                                                           825 AAAAGCACATGACACTTAGTCTTTTGCTGTGCAAATAAGATAAAATGATTTGTCCTTTGT
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  912
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RESULT 2 US-10-750-185-39315/c ; Sequence 39315, Application US/10750185

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SEQ ID NO 39315

; LENGTH: 2464

; TYPE: DNA

ORGANISM: Bovine 198668815642

US-10-750-185-39315
                                                                                                                                                                                                                         APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMI1100-2
CURRENT PLILICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOPTWARE: Patentin version 3.1
SEQ ID NO 49060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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                                                                            Matches
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GENERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.
APPLICANT: DeNISE, Sue K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: MMI GENOMICS, INC. APPLICANT: DENISE, Sue K. APPLICANT: KERR, Richard
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CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
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APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
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                                                                                                                                                                                           TYPE: DNA
                                                                                                                                                                                                             LENGTH: 872
                                                                                            Local Similarity
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                                  316 TTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATGGTTTCCATCACTCTC 375
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  TATTCTCTTATCCACAACCCCACCACCACAAACTCTTTCCCATATTTATTTTCATTGGG 116
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                                                                            Conservative
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                                                                                          3.5%;
                                                                      Score 36; DB 6
Pred. No. 0.61;
0; Mismatches
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Pred. No. 0.48;
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                                                                                                              DB 6; Length 872;
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                                                                          75;
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US-10-750-185-63875/c ; Sequence 63875, Application US/10750185 ; Publication No. US20050260603A1
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APPLICANT: MMI GENOMICS, INC.
APPLICANT: DENISE, Sue K.
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SEQ ID NO 54610
LENGTH: 1012
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Best Local Similarity
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APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: BATES, Stephen
APPLICANT: PANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMII100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR APPLICATION UMMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIN version 3.1
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APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMII100-2
CURRENT FILLING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
PRIOR FILING DATE: 2002-12-31
PRIOR FILING DATE: 2002-12-31
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APPLICANT: DENISE, Sue 1
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, D
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KERR, Richard
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KERR, Richard
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RESULT 7
US-10-821-234-142
; Sequence 142, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
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; ORGANISM: Bovine
US-10-750-185-30880
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US-10-750-185-30880
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; ORGANISM: Bovine
US-10-750-185-63875
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Best Local Similarity
Matches 106; Conserv
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SOFTWARE: PatentIN version 3.1
SEQ ID NO 30880
LENGTH: 1240
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Best Local Similarity
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TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MM11100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
PRIOR FILING DATE: 2002-12-31
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APPLICANT: DENISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
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HOLM, Tom
BATES, Stephen
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CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR FILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
SOFTWARE: pt SEQ_genes Version 1.0
SEQ ID NO 142
LENGTH: 1458
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APPLICANT: PANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMI1100-2
CURRENT FILING DATE: 2003-12-31
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 48714
                                                                                                                          Matches
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Publication No. US20050260603A1
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Best Local Similarity 47.1%;
                                                                                                                                                            Query Match
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APPLICANT: DENISE, Sue F
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, Da
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TITLE OF INVENTION: Methods for Diagnosis
FILE REFERENCE: 821A
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ORGANISM: Homo sapiens
                                                                                                                                                                                                             LENGTH: 2748
TYPE: DNA
ORGANISM: Bovine
                                                                                                                                             Local
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                                                                                                                                             Similarity
DeNISE, Sue K.
KERR, Richard
ROSENFELD, David
HOLM, Tom
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Pred. No. 5;
0; Mismatches
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Pred. No. 3.6;
0; Mismatches 117; Indels
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US-10-750-185-35293
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US-10-750-185-35293
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; ORGANISM: Bovine
US-10-750-185-38532
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Publication No. US20050260603A1
GENERAL INFORMATION:
APPLICANT: WMI GENOMICS, INC.
APPLICANT: DENISE, Sue K.
APPLICANT: KERR, Richard
                                                                                      SOFTWARE: PatentIN version 3.1 SEQ ID NO 35293
Query Match
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Best Local Similarity
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SEQ ID NO 38532
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                                                                                                                             APPLICANT: PANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMILION-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR PILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
                                                                                                                    NUMBER OF SEQ ID NOS: 64922
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                                         TYPE: DNA
ORGANISM: Bovine
                                                                        LENGTH: 973
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Score 33.2;
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Pred. No. 5.3;
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Length 973;
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RESULT 12
US-11-108-172-547/c
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; LOCATION: (216732)..(216833)
; OTHER INFORMATION: C21orf34 exon
US-11-102-978-3
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US-11-102-978-3/c
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APPLICANT: University of Utah Technology Transfer Office
APPLICANT: University of Utah Research Foundation
TITLE OF INVENTION: Diagnosis and Treatment of Herpes Simplex Virus Disease
FILE REFERENCE: 0274-5537.1US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application US/11102978 Publication No. US20050250142A1
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CURRENT FILING DATE: 2005-04-11
PRIOR APPLICATION NUMBER: PCT/US2003/033152
PRIOR FILING DATE: 2003-10-18
PRIOR APPLICATION NUMBER: 60/419,576
PRIOR APPLICATION NUMBER: 60/419,576
PRIOR FILING DATE: 2002-10-18
NUMBER OF SEQ ID NOS: 13
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NUME/REY: exon
LOCATION: (167308)..(210xf34 exon
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TYPE: DNA
ORGANISM: Homo sapiens
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LOCATION: (56948)..(57115)
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                                                                                                                                                                866 CAACTTTTATGATAGCTGTTTT 887
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Pred. No. 98;
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GENERAL INFORMATION:

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RESULT 13
US-10-750-185-58068
US-10-750-185-58068; Application US/10750185; Sequence 58068; Application US/20050266603A1; GENERAL INFORWATION:
; APPLICANT: MMI GENOMICS, INC.; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
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TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.471C15
CURRENT APPLICATION NUMBER: US/11/108,172
CURRENT FILING DATE: 2005-04-15
PRIOR APPLICATION NUMBER: US 10/025,380
PRIOR APPLICATION NUMBER: US 09/922,217
PRIOR APPLICATION NUMBER: US 09/922,217
PRIOR APPLICATION NUMBER: US 09/833,263
PRIOR APPLICATION NUMBER: US 09/833,263
PRIOR APPLICATION NUMBER: US 09/649,811
PRIOR APPLICATION NUMBER: US 09/649,811
PRIOR APPLICATION NUMBER: US 09/649,811
PRIOR APPLICATION NUMBER: US 09/609,448
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Best Local S
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 2000-02-15
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                                                                                                                                                                                                                                      55 TAGAACACCAAGAWRTYTATTAGAAGAAAACTTTTGAGACCTGC
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DeNISE, Sue K.
KERR, Richard
ROSENFELD, David
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Skeiky, )
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Vedvick Thomas S.
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Smith, Carole L.
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Stolk, John A.
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des, Michael J.
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Pred. No. 3.5;
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RESULT 15

US-10-986-501-27/c

; Sequence 27, Application US/10986501

; Publication No. US20050244845A1

; GENERAL INFORMATION:
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LENGTH: 1765
TYPE: DNA
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Best Local &
                                                                                                                                                                                                                                                                           Matches
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SEQ ID NO 58068
LENCTH: 1135
TYPE: DNA
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APPLICANT: FANTIN, Dennis
TITLE OPTINVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMI1100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
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PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: FANYIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMII100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: MMI GENOMICS,
APPLICANT: DENISE, Sue I
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, Da
                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIN version 3.1
                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Bovine 19866880384477
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                                                                                                                                                                                                                                                                                       Match 3.2%;
Local Similarity 64.5%;
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ilarity 64.5%;
Conservative
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 27
LENGTH: 1307
TYPE: DNA
ORGANISM: Homo sapiens
US-10-986-501-27
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Search completed: December Job time: 323.456 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Ruben et al.
TITLE OF INVENTION: 90 Human Secreted Proteins
FILE REFERENCE: PEO13P2C1
CURRENT APPLICATION NUMBER: US/10/986,501
CURRENT FILING DATE: 2004-11-12
PRIOR APPLICATION NUMBER: US/10/621,363
PRIOR FILING DATE: 2003-07-18
PRIOR PILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: 09/969,730
PRIOR FILING DATE: 2001-10-06
PRIOR FILING DATE: 2001-10-06
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PRIOR FILING DATE: 2001-02-01
PRIOR APPLICATION NUMBER: 60/238,291
PRIOR FILING DATE: 2000-10-06
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 09/244,112
PRIOR APPLICATION NUMBER: PCT/US98/16235
PRIOR APPLICATION NUMBER: PCT/US98/16235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Remaining Prior Application data removed - See File Wrapper or PALM.
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PRIOR FILING DATE: 1997-08-19
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APPLICATION NUMBER: 60/056,371
FILING DATE: 1997-08-19
APPLICATION NUMBER: 60/056,732
FILING DATE: 1997-08-19
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                                                                                                                                                                                                                                                                                                                                                                                 590 ATCAACAGGTCCAACAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTTGGAGAATGG
                                                                                              401 AGCCCATTTTTCATCTTCTTTGAAGCATCTTTTAAATATT 362
                                                                                                                               770 TAGGAATTGTTTCCCCTTCTACTGGGCACAATACACGCATT 809
                                                                                                                                                                                        461 ATATTGAACAAGTAAATGGCTCCTTCTCCTGAACAGGGGTTAACCAGTTTTACAAACATT
                                                                                                                                                                                                                                     710 CTATTCCATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGC 769
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1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*

3: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*

4: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*

5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*

6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

7: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

9: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

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9: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
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Maximum Match 100%
Listing first 45 summaries
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Copyright (c) 1993 - 2005
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 US-10-696-639-15
US-10-408-009-1
US-10-857-785-1
US-10-856-109-1
US-10-856-109-1
US-10-856-109-1
US-10-753-195-1
US-10-753-195-1
US-10-753-143-678
US-10-861-662-878
US-09-789-669-878
US-09-789-679-878
US-09-895-793-878
US-09-895-793-878
US-10-011-095-1
US-10-011-095-1
US-10-011-095-1
US-10-1010-667A-1
US-10-1010-667A-1
US-10-1010-667A-1
US-10-1010-667A-1
US-10-104-679A-1
US-10-393-567-35
US-10-393-567-35
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Sequence 2, Appli
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Sequence 36, Appli
Sequence 378, App
Sequence 35, Appl
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US-10-010-667A-6	US-10-011-095-6	US-10-861-662-10	US-10-830-899-10	US-10-861-662-6	US-10-830-899-6	US-10-723-860-5120	US-10-755-889-191	US-09-814-353-19910	US-10-425-114-16445	US-11-051-454-396	US-10-631-467-428	US-10-858-887-1	US-10-956-157-7046	US-10-956-157-1811	US-10-948-518-42	US-10-948-518-16	US-10-750-262-1	US-10-643-795A-42	US-10-643-795A-16	US-10-295-027-1130	US-10-295-027-713
Sequence 6, Appli	Sequence 6, Appli	Sequence 10, Appl	Sequence 10, Appl	Sequence 6, Appli	Sequence 6, Appli	Sequence 5120, Ap	Sequence 191, App	Sequence 19910, A	Sequence 16445, A	Sequence 396, App	Sequence 428, App	Sequence 1, Appli	Sequence 7046, Ap	Sequence 1811, Ap	Sequence 42, Appl	Sequence 16, Appl	Sequence 1, Appli	Sequence 42, Appl	Sequence 16, Appl	Sequence 1130, Ap	Sequence 713, App

ALIGNMENTS

RESULT 1 US-10-696-639-15

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CURRENT APPLICATION NUMBER: US/10/696,639
; CURRENT FILING DATE: 2003-10-29
; PRIOR APPLICATION NUMBER: 60/422,176
; PRIOR APPLICATION NUMBER: 60/422,176
; PRIOR FILING DATE: 2002-10-9
; NUMBER OF SEQ ID NOS: 3114
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 15
; LENGTH: 1177
; TYPE: DNA
; ORGANISM: homo sapiens
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Publication No. US20050037439A1
GENERAL INFORMATION:
APPLICANT: Pharmacia Corporation
APPLICANT: Bourner, Maureen J.
TITLE OF INVENTION: DIFFERENTIALLY EXPRESSED GENES INVOLVED IN CANCER, THE
TITLE OF INVENTION: POLYPEPTIDES ENCODED THEREBY, AND METHODS OF USING THE SAME
FILE REFERENCE: 01040/1
                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 1017; Conserv
306
                                   241
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RESULT 2

US-10-165-044-1

Sequence 1, Application US/10165044

Publication No. US20030149531A1

GENERAL INFORMATION:
APPLICANT: Rene S. Hubert
APPLICANT: Arthur B. Raitano
APPLICANT: Daniel E. H. Afar
APPLICANT: Daniel E. H. Afar
APPLICANT: Steven Chappell Mitchell
APPLICANT: Mary Faris
APPLICANT: Aya Jakobovits

TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
TITLE OF INVENTION NUMBER: US/10/165,044

CURRENT APPLICATION NUMBER: US 60/087,520
PRIOR APPLICATION NUMBER: US 60/097,183
PRIOR APPLICATION NUMBER: US 60/091,183
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PRIOR FILING DATE: 1999-12-06
PRIOR APPLICATION NUMBER: WO 99/62941
PRIOR FILING DATE: 1999-06-01
PRIOR APPLICATION NUMBER: PCT/US00/33040
PRIOR FILING DATE: 2000-12-06
NUMBER OF SEQ ID NOS: 57
SOFTWARE: FastSEQ for Windows Version 4.0
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US-10-408-009-1
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Publication No. US20040072196A1
GENERAL INFORMATION:
APPLICANT: Daniel E. Afar
APPLICANT: Rene S. Hubert
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PRIOR FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 1
ENGTH: 1193
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Best Local
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CURRENT APPLICATION NUMBER: US/10/408,009
CURRENT FILING DATE: 2003-04-04
PRIOR APPLICATION NUMBER: 09/455,486
PRIOR FILING DATE: 1999-12-06
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APPLICANT: Arthur B. Raitano
APPLICANT: Douglas C. Saffran
APPLICANT: Stephen C. Mitchell
TITLE OF INVENTION: MOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY: CDS
LOCATION: (64)...(1083)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo
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Local Similarity 100.0%;
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Pred. No. 7e-277;
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                                             APPLICANT: Daniel E. Afar
APPLICANT: Paniel E. Hubert
APPLICANT: Rene S. Hubert
APPLICANT: Arthur B. Raitano
APPLICANT: Douglas C. Saffran
APPLICANT: Stephen C. Mitchell
TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREO
FILE REFERENCE: 51152001607
CURRENT APPLICATION NUMBER: US/10/857,785
CURRENT FILING DATE: 2004-05-28
PRIOR APPLICATION NUMBER: US 09/455,486
PRIOR APPLICATION NUMBER: US 09/33,873
PRIOR FILING DATE: 1999-06-01
PRIOR FILING DATE: 1999-06-01
PRIOR APPLICATION NUMBER: US 60/087,520
PRIOR APPLICATION NUMBER: US 60/091,183
PRIOR PILING DATE: 1998-06-30
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                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/10857785 Publication No. US20040219162A1 GENERAL INFORMATION:
 SEQ ID
 NUMBER OF SEQ ID 1
SOFTWARE: FastSEQ
SEQ ID NO 1
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; LENGTH: 1193
; TYPE: DNA
; ORGANISM: Homo sap:
; ERATURE:
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; NAME/KEY: CDS
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GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT
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APPLICANT: Daniel E. Afar
APPLICANT: Rene S. Hubert
APPLICANT: Arthur B. Raitano
APPLICANT: Arthur B. Raitano
APPLICANT: Douglas C. Saffran
APPLICANT: Stephen C. Mitchell
TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
TITLE OF INVENTION: NOVEL SERPENTIN HUMAN CANCERS AND USES THEREO
FILE REFERENCE: 511582001606
CURRENT APPLICATION NUMBER: US 09/455,486
PRIOR APPLICATION NUMBER: US 09/455,486
PRIOR APPLICATION NUMBER: US 09/323,873
PRIOR FILING DATE: 1999-06-01
PRIOR APPLICATION NUMBER: US 60/087,520
PRIOR APPLICATION NUMBER: US 60/091,183
PRIOR FILING DATE: 1998-06-03
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US-10-856-109-1
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Best Local S
Matches 1017
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SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 1
LENGTH: 1193
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Publication No. US20040219591A1
GENERAL INFORMATION:
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LOCATION: (64)...(1083)
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nes 1017; Conserv
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                       GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA
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US-10-830-899-2

Sequence 2, Application US/10830899

Publication No. US20040253232A1

GENERAL INFORMATION:

APPLICANT: Jakobovits, Aya

APPLICANT: Etessami, Soudabeh

APPLICANT: Heresami, Soudabeh

APPLICANT: Faris, Mary

APPLICANT: Faris, Mary

APPLICANT: Raitano, Arthur B.

TITLE OF INVENTION: Antibodies and Molecules Der.

TITLE OF INVENTION: therefrom that Bind to STEAN

FILE REFERENCE: 51158-20016.26

CURRENT APPLICATION NUMBER: US/10/830,899

CURRENT APPLICATION NUMBER: 09/323,873

PRIOR APPLICATION NUMBER: 10/010,667

PRIOR APPLICATION NUMBER: 10/010,667

PRIOR APPLICATION NUMBER: 10/011,095

PRIOR FILING DATE: 2001-12-06

PRIOR APPLICATION NUMBER: 10/236,878

PRIOR APPLICATION NUMBER: 09/455,486

PRIOR APPLICATION NUMBER: 09/455,486

PRIOR FILING DATE: 1999-12-06

PRIOR APPLICATION NUMBER: 60/091,183

PRIOR FILING DATE: 1999-12-06

PRIOR APPLICATION NUMBER: 60/091,183

PRIOR FILING DATE: 1999-12-06

PRIOR APPLICATION NUMBER: 60/091,183

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; SOFTWARE: FASTSEQ for Windows Ve; SEQ ID NO, 2
; SEQ ID NO, 2
; LENGTH: 1193
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (66)...(1085)
US-10-830-899-2
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PRIOR APPLICATION NUMBER: US 09/453,195
PRIOR APPLICATION NUMBER: US/10/165,044
PRIOR FILING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: US 60/087,520
PRIOR FILING DATE: 1998-06-01
PRIOR APPLICATION NUMBER: US 60/091,183
PRIOR APPLICATION NUMBER: US 60/091,183
PRIOR APPLICATION NUMBER: US 09/323,873
PRIOR APPLICATION NUMBER: US 09/323,873
PRIOR FILING DATE: 1999-06-01
PRIOR APPLICATION NUMBER: US 09/455,486
PRIOR APPLICATION NUMBER: WO 99/62941
PRIOR APPLICATION NUMBER: WO 99/62941
PRIOR APPLICATION NUMBER: WO 99/62941
PRIOR FILING DATE: 1999-06-01
PRIOR APPLICATION NUMBER: WO 99/62941
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                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 1017; Conserv
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SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Agensys, Inc.
APPLICANT: Rene S. Hubert
APPLICANT: Arthur B. Raitano
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: 51158-20016.02
CURRENT APPLICATION NUMBER: US/10/753,195
CURRENT FILING DATE: 2004-01-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THE FILE REFERENCE: 51158-20016.02
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APPLICANT:
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                                                                                                                                                                                                                                                                                             NAME/KEY: CDS
LOCATION: (64)...(1191)
                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Homo
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                 CTTCAGCACACAGAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT
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APPLICANT: Daniel E. Afar
APPLICANT: Daniel E. Hubert
APPLICANT: Rene S. Hubert
APPLICANT: Arthur B. Rattano
APPLICANT: Douglas C. Saffran
APPLICANT: Stephen C. Mitchell
TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THE
FILE REFERENCE: 511582001612
CURRENT APPLICATION NUMBER: US/10/752,421
CURRENT FILING DATE: 2004-01-05
PRIOR APPLICATION NUMBER: US 09/455,486
PRIOR FILING DATE: 1999-12-06
PRIOR APPLICATION NUMBER: US 09/323,873
PRIOR FILING DATE: 1999-06-01
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; LOCATION: (64)...
US-10-752-421-1
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Best Local Similarity 100.
Matches 1017; Conservative
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PRIOR FILING DATE: 1998-06-01
PRIOR APPLICATION NUMBER: US 60/091,183
PRIOR FILING DATE: 1998-06-30
NUMBER OF SEQ ID NOS: 47
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ORGANISM: Homo sapiens
FEATURE:
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100.0%; Pred. No. 7e-277;
tive 0; Mismatches 0;
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; LENGTH: 1193
; TYPE: DNA
; ORGANISM: Homo sapiens
; PEATURE:
; NAME/KEY: CDS
; LOCATION: (66)...(1085)
US-10-861-662-2
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APPLICANT: Gudas, Jean
APPLICANT: Gudas, Jean
APPLICANT: Raitano, Arthur B.
TITLE OF INVENTION: Antibodies and Molecules Derived
TITLE OF INVENTION: Cherefrom that Bind to STEAP-1 Proteins
FILE REFERENCE: 51158-20016-16.
CURRENT APPLICATION NUMBER: US/10/861,662
CURRENT FILING DATE: 2004-06-04
PRIOR APPLICATION NUMBER: 09/23,873
PRIOR FILING DATE: 199-06-01
PRIOR APPLICATION NUMBER: 10/010,667
PRIOR APPLICATION NUMBER: 10/010,95
PRIOR FILING DATE: 2001-12-06
PRIOR APPLICATION NUMBER: 10/011,095
PRIOR APPLICATION NUMBER: 10/015,486
PRIOR APPLICATION NUMBER: 09/455,486
PRIOR APPLICATION NUMBER: 09/091,183
PRIOR FILING DATE: 1998-06-30
NUMBER OF SEQ ID NOS: 103
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APPLICANT: Etessami, Soudat
APPLICANT: Challita-Eid, Pi
APPLICANT: Perez-Villar, Ju
APPLICANT: Meyrick Morrisor
APPLICANT: Jia, Xiao-Chi
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SEQ ID NO 2
LENGTH: 1193
                                                                                                                                                                                                                                                   Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 1017; Conservative 0
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Publication No. US20050086707A1
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Challita-Eid, Pia M.
Perez-Villar, Juan
Meyrick Morrison, Karen J
Jia, Xiao-Chi
                        CCTGTGCTTTTGCATTTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA
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CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA
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Pred. No. 7e-277;
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US-09-759-143-878
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PATENT NO. US2007
GENERAL INFORMAT:
APPLICANT: Mitch
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APPLICANT: Harx
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APPLICANT: Henr
APPLICANT: Kale
APPLICANT: Reti
APPLICANT: Sto.
APPLICANT: Sto.
APPLICANT: Sto.
Sequence 878, Application US/09759143
Patent NO. US20022248A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Rater, Marc W.
APPLICANT: Retter, Marc W.
APPLICANT: Retter, Marc W.
APPLICANT: Retter, Marc W.
APPLICANT: Boy, Craig H.
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APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
APPLICANT: Mang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
TITLE OF INVENTION UNMBER: US/09/759,143
CURRENT APPLICATION NUMBER: US/09/759,143
CURRENT APPLICATION NUMBER: US/09/759,143
CURRENT FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 934
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 878
LENGTH: 1195
TYPE: DNA
ORGANISM: Homo sapiens
US-09-759-143-878
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     GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT
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                                         TCTCTGGGAATTGTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT
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GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin (
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US-09-780-669-878
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SOFTWARE: FastSEQ for
SEQ ID NO 878
LENGTH: 1195
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                                                                                                                                                                                                                                                                                                                                               APPLICANT: MCNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C24
CURRENT APPLICATION NUMBER: US/09/780,669
CURRENT FILING DATE: 2001-02-09
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Skeiky, Yasir A.W.
Hepler, William
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                                                                    AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA
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Retter, Marc W.
Stolk, John A.
Day, Craig H.
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Mitcham, Jennifer
Harlocker, Susan I
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       Sequence 878, Application US/09822827

Patent No. US20020081680A1

GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
ITITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.534C1
CURRENT APPLICATION NUMBER: US/09/822,827
CURRENT FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 982
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 878
LENGTH: 1195
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CURRENT FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 982
SOFTWARE: FRASTSEQ for Windows Version 3.0
SEQ ID NO 878
LENGTH: 1195
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER FILE REFERENCE: 210121.534C2
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Skeiky, Yasir A.W.
Hepler, William T.
Henderson, Robert A
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GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA
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                                                 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG
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Houghton, Raymond L.
Vinals de Bassols, C
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Kalos, Michael D.
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Vedvick, Thomas S
Carter, Darrick
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Pred. No. 7e-277;
0; Mismatches 0;
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US-UY-BYS-B14-B78

; Sequence 878, Application US/09895814

; Publication No. US2020193296A1

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Dillon, Davin C.

; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: Harlocker, Susan L.

; APPLICANT: Harlocker, Susan L.

; APPLICANT: Kalos, Michael D.

; APPLICANT: Stolk, John A.

; APPLICANT: Vedvick, Thomas S.

; APPLICANT: Vedvick, Thomas S.

; APPLICANT: Vedvick, Thomas S.

; APPLICANT: Wang, Aijun

; APPLICANT: Wang, Aijun

; APPLICANT: Henderson, Robert A.

; APPLICANT: Wang, Aijun

; APPLICANT: Winals de Bassols, Carlota

; APPLICANT: Vinals de Bassols, Carlota

; APPLICANT: Foy, Teresa

; APPLICANT: Fonger, Gary R.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THEI

; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

; FILE REFERENCE: 210121.427C26
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US-09-895-814-878
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; ORGANISM: Homo
US-09-895-814-878
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CURRENT FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 990
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 878
LENGTH: 1195
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          CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG
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APPLICANT: Fanger, Gary R.
APPLICANT: Wantanabe, Yoshihiro
APPLICANT: Meagher, Madelline Joy
APPLICANT: Meagher, Madelline Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C27
CURRENT APPLICATION NUMBER: US/10/012,896
CURRENT FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 1011
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 878
LENGTH: 1195
TYPE: DNA
TYPE: DNA
HOMO sapiens
US-10-012-896-878
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US-10-012-896-878
US-10-012-896-878
Sequence 878, Application US/10012896
Publication US20020183251A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              901
                                     246
                                                                       181
                                                                                                         186 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA
                                                                                                                                            121
                                                                                                                                                                                  126 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA
241 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 300
                                                                                                                                                                                                       61 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA
                                                                                                                                                                                                                                                      66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jiang, Yuqiu
Kalos, Michael D.
Retter, Marc W.
Stolk, John A.
Day, Craig H.
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                                                                                                                                                                                                                                                      ATGGAAAGCAGAAAAGACATCACAAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA
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                                                        CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT
                                                                                                                               CCTGTGCTTTTGCATTTGCACCAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 180
                                     CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT
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Houghton, Raymond L.
Vinals de Bassols, Carlota
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Hepler, William T.
Henderson, Robert A.
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Mitcham, Jennifer L.
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Li, Samuel X.
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                                       305
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Вb	306	4.
Qy	301	TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 360
Db	366	TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 425
δ	361	GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 420
Db	426	GTTTCCATCACTCTTTGGCATTGGTTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 485
Ş	421	CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGG
Ъ	486	CTTCATAATGGAACCAAGTATAAGAAGTTTCCACACTTGGTTGG
γQ	481	AGAAAGCAGTTTGGGCTTCTCAGTTTTCTTTTTTGCTGTACTGCATGCA
дd	546	AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTTGCTGTACTGCATGCA
δ	541	TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 600
Db	606	TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 665
.8	601	CAACAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTTGGAGAATTGAGAGATTTATGTG 660
ф	666	CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTTGGAGAATGGAGATTTATGTG 72
Ş	661	TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 720
Ъ	726	TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 785
δ	721	GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 780
σb	786	GTGAGTGACTCTTTGACATGGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 845
ફ	781	TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATA
Db	846	TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATA
Ş	841	AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCC
Вb	906	AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCC
δ	901	GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 96
Db	966	GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 102
ş	961	AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1017
Дb	1026	

Search completed: December 5, 2005, 07:54:11 Job time : 952.415 secs

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Database
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1: /cgm2_6/ptodata/1

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/cgn2_6/ptcdata/1/ina/6_COMB.seq:*
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/cgn2_6/ptcdata/1/ina/PCTUS_COMB.seq:*
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/cgn2_6/ptcdata/1/ina/RE_COMB.seq:*
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US-09-455-667A-6
US-09-455-667A-6
US-09-455-66A-342
US-09-455-16A-342
US-09-651-236-342
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Sequence 342, App
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Result

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ALIGNMENTS

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; LENGTH: 1193
; TYPE: DNA
; ORGANISM: Homo sapiens
; PEATURE:
; NAME/KEY: CDS
; LOCATION: (64)...(1083)
US-09-455-486-1
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APPLICANT: Rene S. Hubert
APPLICANT: Arthur B. Raitano
APPLICANT: Douglas C. Saifran
APPLICANT: Douglas C. Saifran
APPLICANT: Stephen C. Mitchell
TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANT
TITLE OF INVENTION: REPRESSED IN HUMAN CANCERS AND USE
FILE REFERENCE: 129.17-US-I1
CURRENT APPLICATION NUMBER: US/09/455,486
CURRENT FILING DATE: 1999-12-06
PRIOR APPLICATION NUMBER: 09/323,873
PRIOR APPLICATION NUMBER: 09/323,873
PRIOR FILING DATE: 1999-06-01
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 1017; DB 3; Best Local Similarity 100.0%; Pred. No. 2.5e-304; Matches 1017; Conservative 0; Mismatches 0;
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SOFTWARE: FastSEQ for
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FastSEQ for Windows Version
CTTCAGCACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT
                                                                                                                  CCTGTGCTTTTGCACTTTGCACCAAACAGCCCATGCTGAATTTGAACTTGCCCCTTCAGAA 180
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Sequence 1, Application US/09323873A

Patent No. 6329503

GENERAL INFORMATION:

APPLICANT: Daniel E. Afar

APPLICANT: Rene S. Hubert

APPLICANT: Arthur B. Raitano

APPLICANT: Arthur B. Raitano

APPLICANT: Douglas C. Saffran

APPLICANT: NOVEL SERPENTINE TRANSMEMERANE ANTIGENS

TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMERANE ANTIGENS

TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMERANE ANTIGENS

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APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
ITILE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
ITILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C21
CURRENT APPLICATION NUMBER: US/09/685,166A
CURRENT FILING DATE: 2000-10-10
NUMBER OF SEQ ID NOS: 898
SOPTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 878
LENGTH: 1195
TYPE: DNA
ORGANISM: Homo sapiens
US-09-685-166A-878
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APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer
APPLICANT: Harlocker, Susan L
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Kalos, Michael D
Fanger, Gary R.
Retter, Marc W.
Stolk, John A.
Day, Craig H.
Vedvick, Thomas !
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             APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHOI
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE (
TILE REFERENCE: 210121.427C20
CURRENT APPLICATION NUMBER: US/09/679,426
CURRENT FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 895
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Kalos, Michael D.
Fanger, Gary R.
Retter, Marc W.
Stolk, John A.
Day, Craig H.
Vedvick, Thomas &
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Dillon, Davin C.
Mitcham, Jennifer L.
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APPLICANT: Mitcham, Jewin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Kalos, Michael D.
APPLICANT: Kalos, Michael D.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Wang, Aijun
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHOD:
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE C:
FILE REFERENCE: 210121.427C23
CURRENT FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 934
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 878
LENGTH: 1195
TYPE: DNA
ORGANISM: Homo sapiens
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Mitcham, Jennifer
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APPLICANT: Hubert, Rene S.

APPLICANT: Hubert, Rene S.

APPLICANT: Leong, Kahan

APPLICANT: Saffran, Arthur B.

APPLICANT: Saffran, Douglas C.

APPLICANT: Mitchell, Steve Chappell

TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS

TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS

TITLE OF INVENTION: NUMBER: US/10/010,667A

CURRENT APPLICATION NUMBER: 09/323,873

PRIOR APPLICATION NUMBER: 09/323,873

PRIOR APPLICATION NUMBER: 60/087,520

PRIOR APPLICATION NUMBER: 60/087,520

PRIOR APPLICATION NUMBER: 60/091,183

PRIOR APPLICATION NUMBER: 60/091,183

PRIOR FILING DATE: 1998-06-30

NUMBER OF SEQ ID NOS: 32

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 1

LENGTH: 1195

TYPE: DNA

ORGANISM: Homo Sapiens
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US-10-010-667A-1
US-10-010-667A-1
; Sequence 1, Application User 1, Septent No. 6887975
; Patent No. 6887975
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Patent No. 6943236
GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 1017; Conservative
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 878
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C27
CURRENT APPLICATION NUMBER: US/10/012,896
CURRENT FILING DATE: 2001-12-10
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                                          GTTTCCATCACTCTTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA
                                                                                                       TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG
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TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG
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Meagher, Madeleine Joy
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Houghton, Raymond L.
Vinals de Bassols, Carlota
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Vedvick, Thomas S
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Stolk, John A.
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Mitcham, Jennifer L.
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Hepler, William T.
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Li, Samuel X.
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Pred. No. 2.5e-304;
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PRIOR FILING DATE: 2000-10-20
PRIOR PELICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR EILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASTSEQ for Windows Version 4.
SEQ ID NO 2686
LENGTH: 1147
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US-09-949-016-2686
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Sequence 2686, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: FOLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                         Query Match
Best Local Similarity
Matches 1016; Conserv
                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
                                                                                                                                                   TYPE: DNA
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                  ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 60
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 ATGGAAAGCAGAAAAGACATCACAAAACCAAGAAGTTTTGGAAAATGAAGCCTTAGGAGA
                                                            Conservative
                                                                          99.8%;
99.9%;
                                                            <u>.</u>
                                                                          Score 1015.4;
Pred. No. 7.86
                                                              Mismatches
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RESULT 9
US-09-323-873A-6
US-09-323-873A-6
; Sequence 6, Application US/09
; Patent No. 6329503
; GENERAL INFORMATION:
; APPLICANT: Daniel E. Afar
; APPLICANT: Rene S. Hubert
; APPLICANT: Kahan Leong
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Arthur B. Raitano
APPLICANT: Douglas C. Saffran
APPLICANT: Steve Chappell Mitchell
APPLICANTON: EXPRESED IN HUMAN CANCERS AND USES THEREOF
FILE REPERENCE: 129.16USU2
CURRENT APPLICATION NUMBER: US/09/323,873A
CURRENT FILING DATE: 1999-06-01
PRIOR APPLICATION NUMBER: 60/087,520
PRIOR APPLICATION NUMBER: 60/087,520
PRIOR APPLICATION NUMBER: 60/087,520
PRIOR APPLICATION MIMBER: 60/087,520
PRIOR FILING DATE: 1998-06-30
NUMBER OF SEQ ID NOS: 32
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; SEQ ID NO 6
; LENGTH: 3627
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-09-323-873A-6
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Best Local Sim:
Matches 763;
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   GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAA
                    CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG
                                                                                                           TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC
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Pred. No. 1.2e-224;
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SOFTWARE: FASTSEQ for Wi
SEQ ID NO 4
LENGTH: 3627
TYPE: DNA
ORGANISM: Homo sapiens
US-09-455-486-4
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APPLICANT: Rene S. Hubert
APPLICANT: Arthur B. Raitano
APPLICANT: Douglas C. Saffran
APPLICANT: Douglas C. Saffran
APPLICANT: Stephen C. Mitchell
TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF
FILE REFERENCE: 129.17-US-11
CURRENT APPLICATION NUMBER: US/09/455,486
CURRENT FILING DATE: 1999-12-06
PRIOR APPLICATION NUMBER: 09/323,873
PRIOR FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 34
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Best Local Similarity
Matches 763; Conserv
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TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC
                                                      CTTCAGCACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT
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Pred. No. 1.2e-224;
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Afar, Daniel
APPLICANT: Habert, Rene S.
APPLICANT: Leong, Kahan
APPLICANT: Leong, Kahan
APPLICANT: Raitano, Arthur B.
APPLICANT: Saffran, Douglas C.
APPLICANT: Mitchell, Steve Chappell
APPLICANT: Mitchell, Steve Chappell
APPLICANT: Mitchell, Steve Chappell
TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF
FILE REFERENCE: 511582001601
CURRENT FILING DATE: 2001-12-06
PRIOR APPLICATION NUMBER: US/10/010,667A
CURRENT FILING DATE: 1999-06-01
PRIOR APPLICATION NUMBER: 60/087,520
PRIOR APPLICATION NUMBER: 60/087,520
PRIOR FILING DATE: 1998-06-01
PRIOR FILING DATE: 1998-06-01
PRIOR FILING DATE: 1998-06-30
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 6
LENGTH: 3627
TYPE: DNA
ORGANISM: Homo sapiens
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Local Similarity 99.5%;
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GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA
                                                           TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG
                                                                                TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG
                                                                                                                                    ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCCTTAGCAACT
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Pred. No. 1.2e-224;
0; Mismatches 4;
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; ORGANISM: Homo sapien
US-09-439-313-342
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US-09-439-313-342/c
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APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan Lou
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CURRENT FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 575
SOFTWARE: FRANCSEQ for Windows Version 3.0
SEQ ID NO 342
LENGTH: 592
                                                                                                                                                                    Query Match
Best Local Similarity
Matches 516; Conserv
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                                                                                                                                                                                                                                                                                                                           APPLICANT: Solk, John
APPLICANT: Day, Craig
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C9
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                                            CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 180
                                                                      AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA
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Reed, Steven G.
Kalos, Michael
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CTTCAGCACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT
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Retter, Mark
                                                                                                                                                                     Conservative
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RESULT 13
US-09-352-616A-342/c
; Sequence 342, Application US/09352616A
; Patent No. 639527B
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SEQ ID NO 342
LENGTH: 592
TYPE: DNA
ORGANISM: Homo sapien
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APPLICANT: Dillon, Davin C.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Harlocker, Susan Louise
APPLICANT: Jiang, Yuqni
APPLICANT: Xu, Jiangchun
APPLICANT: Mitcham, Jennifer Lynn
APPLICANTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR U
FILE REPERENCE: 201011.42708
CURRENT APPLICATION UMBER: US/09/352,616A
CURRENT FILING DATE: 1999-07-13
NUMBER OF SEQ ID NOS: 472
SOFTWARE: PESTED FOR WINDOWS Version 3 0
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Best Local Similarity 99.6%;
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TCCCATCAACAATATTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG
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Pred. No. 2.4e-149;
1; Mismatches 1;
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RESULT 14
US-09-636-215-342/c
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CURRENT APPLICATION NUMBER: US/09/636,215
CURRENT FILLING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 852
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 342
LENGTH: 592
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APPLICANT:
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APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.42717C17
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Retter, Marc W.
Stolk, John A.
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Vedvick, Thomas S.
Carter, Darrick
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Dillon, Davin C.
Mitcham, Jennifer L.
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Kalos, Michael D.
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99.6%;
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Pred. No. 2.4e-149;
1; Mismatches 1;
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER FILE REFERENCE: 210121.427C21
CURRENT APPLICATION NUMBER: US/09/685,166A
CURRENT APPLICATION NUMBER: US/09/685,166A
CURRENT FILING DATE: 2000-10-10
NUMBER OF SEQ ID NOS: 898
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 342
LENGTH: 592
Type. ....
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US-09-685-166A-342/c
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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqui
APPLICANT: Kalos, Michael D.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Vedvick, Thomas S.
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Best Local S
Matches 516
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CTTCAGCACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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The invention relates to an antibody immunospecifically binds to p-cadherin or its fragment. The antibody is useful in preparing a composition for treating or preventing a cancer-associated disorder. present sequence represents a gene upregulated in human colon cancer cells.

The

Disclosure; SEQ ID NO 15; 257pp; English.

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CC This sequence represents cDNA encoding a novel human protein, STRAP-1 CC (serpentine transmembrane antigen of the prostate). STRAP-1 is the CC prototype member of the STRAP family of proteins (AAY58194-Y58197) which CC exhibit a high degree of structural conservation, but which show no CC significant structural homology to known human proteins. The STRAP-1 gene CC lila membrane protein and is expressed predominantly in prostate cells in CC cornal human tissues. Structurally, STRAP-1 is a 339 amino acid protein CC caracterised by six transmembrane domains and intracellular N- and C-CC termini, suggesting that it folds in a "serpentine" manner into three CC extracellular and two intracellular loops. STRAP-1 mRNA and protein CC expression is maintained at high levels and throughout all stages of CC prostate cancer. STRAP-1 mRNA and/or protein is also overexpressed in CC certain other cancers, including bladder, colon, pancreatic and ovarian cancer. The function of the STRAP proteins is not known. They may be ion CC channels (from the presence of six transmembrane domains, a feature which is shared by certain ion channels) or gap-junction proteins (from the context of the strap context of the strap cancer are cell-surface tumour antigens. Immunisation with a STRAP protein induces cellular and

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Fig 1A; 83pp;

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The present sequence is human six transmembrane epithelial antigen of the prostate (STRAP): I clone 10 cDNA. STRAP is a member of cell surface serpentine transmembrane antigens. STRAP is a member of cell surface pp.22.3 and is used in gene therapy. Inhibiting the development or progression of a cancer (eg. prostate, colon, bladder, lung, ovarian and pancreatic) expressing STRAP or inhibiting growth or killing cells expressing STRAP in a patient, comprises administering a vaccine composition to the patient. Treating a patient with a cancer that
                                                                                                                                                                                                                          Afar DEH,
Faris M,
                                                                                                                                                New STEAP proteins,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; cytostatic; antiproliferative; vaccine; gene therapy; six transmembrane epithelial antigen of the prostate-1; STEAP-1; chromosome 7p22.3; cancer; prostate; colon; bladder; lung; ovarian; pancreatic; ss.
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P-PSDB; AAE02780.
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Jakobovits
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                                                                                                                                                                                                                                                                                                                                                                                                 the prostate (STEAP) .1"
/note= "CDS does not include stop codon"
/transl except= [pos:1078. .1086, aa:Leu-Asn)
/note= "Inframe stop codon alters the reading
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers 64. .1191
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Pred. No. 2.6e-276;
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                                                                                                                                                              Query Match
Best Local Similarity
Matches 1017; Conserv
                                                                                                                                                                                                                                                                                                                                                                                      The invention describes a composition comprising a substance that modulates the status of a protein (I) of 340 or 283 amino acids, or of any of the 15 sequences of 259 amino acids, given in the specification, or a molecule that is modulated by the protein, where the status of the cell that expresses the protein is modulated. The compositions, proteins polynucleotides and methods are useful for treating and detecting cancer The STEAP-1-related proteins are useful for generating cancer vaccines. The polynucleotides are useful as tools for delineating, with greater precision, cytogenetic abnormalities in the chromosomal region that encodes STEAP-1 that may contribute to the malignant phenotype. This sequence encodes a variant of human six transmembrane epithelial antigen of the prostate or STEAP-1
                                                                                                                                                                                                                                                                                                                       Sequence 1193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New composition comprising a substance that modulates the status of STEAP-1-related protein, useful for treating and detecting cancer.
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05-APR-2002; 2002US-0370387P.
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                                                                                                                     AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG
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                                                                                                                                                   Query Match
Best Local Similarity
Matches 1017; Conserv
                                                                                                                                                                     The invention relates to cell surface serpentine transmembrane antigens predominantly expressed in the prostate termed as six transmembrane epithelial antigen of prostate (STEAP-2) and their corresponding nucleic acid sequences. STEAP-2 DNA is useful for diagnosing or treating prostate cancer. It can be used as a primer or probe for the amplification and/or detection of STEAP genes and as a tool for modulating or inhibiting the expression of the STEAP genes. STEAP-2 DNA is also useful in cancer vaccines for the generation of therapeutic or prophylactic immunity against prostate cancer. STEAP antibodies are useful in antibody therapy. The present sequence is the human STEAP-1 cDNA. Human STEAP-1 gene maps within chromosome 7p22 (7p2.3).
                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                   Novel isolated polynucleotide that encodes six transmembrane epithelial antigen of prostate polypeptide, useful for diagnosing or treating
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06-DEC-1999;
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) HUBERT R S.
) RAITANO A B.
) SAFFRAN D.
) MITCHELL S C.
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AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA
              AATTTAGAAGAAGAAGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA
                                                ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA
                                                               ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA
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ilarity 100.0%;
Conservative (
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Pred. No. 2.6e-276;
Mismatches 0;
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CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA

CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA

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RESULT 6
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Matches 1017
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Xu J, Dillon DC, Mit Kalos MD, Fanger GR, Wang A, Meagher MJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New polynucleotide encoding a prostate-specific protein, monitoring and treating prostate cancer in a patient and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-JAN-2000; 2000US-00483672
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Xu J, Dillon
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Li SX, Wang
The invention relates to isolated prostate-specific polynucleotides, polypeptides, fusion proteins of the polypeptides, antibodies raised against the polypeptides (or antigenic epitopes derived from them) and antigen-presenting cells expressing the polypeptides. The antibodies are useful for detecting the presence of cancer, especially prostate cancer. The polypeptides, polynucleotides and the antigen-presenting cells are useful for stimulating and/or expanding T cells specific for a tumour protein, and for inhibiting the development of cancer especially prostate cancer. Compositions comprising the polynucleotide and/or polypeptide are useful for stimulating an immune response, and for treating cancer. The oligonucleotide is useful for detecting cancer. The present sequence is a prostate specific polynucleotide of the invention
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P-PSDB; AAU69927.
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Sequence 1195 BP; 382 A; 221 C; 233 G; 359

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                   WANG A.

SKEIKY Y A W.

HEPLER W T.

HENDERSON R A.
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DAY C H.
VEDVICK T S.
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KALOS M D.
FANGER G R.
RETTER M W.
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DILLON D
MITCHAM
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HARLOCKER S L.
                                                                                                                             CARTER D.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 1017;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention describes a fusion protein comprising at least one amino acid sequence of immunogenic portions of any of the 3 sequences not defined in the specification, or sequences having at least 70 or 90 % sequence identity to any one of the 35 sequences defined in the USPTO web site, which is encoded by any of the 4 nucleotide sequences not defined in the specification. The fusion protein, composition and methods are useful for diagnosing, preventing and/or treating cancer, particularly prostate cancer. The proteins are useful as markers to indicate the presence or absence of cancer. This sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the US patent office at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fanger
Li SX,
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(HOUG/)
(DBAS/)
(FOYT/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 5; SEQ ID NO 878;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Prostate specific protein and its encoding treatment and diagnosis of prostate cancer
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PD, Houghton
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GTTTCCATCACTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA
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                                                                                                                                                                                                                                                                                                          New prostate-specific polynucleotides for diseases, in particular prostate cancer, progression of cancer.
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Fanger
Li SX,
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06-SEP-2000;
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GR, Retter MW, Stolk JA,
Wang A, Skeiky YAW, Hep
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DILLON D C.
MITCHAM J L.
HARLOCKER S I
JIANG Y.
KALOS M D.
FANGER G R.
RETTER M W.
STOLK J A.
DAY C H.
DAY C H.
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JA, Day CH, Vedvick T
Hepler WT, Henderson F
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gene therapy; gene; ds.
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                                                                                                                                                            Detecting a prostate cancer-associated transcript in a cell in a patient, useful for diagnosing prostate cancer (PC) or screening modulators of PC, by determining if prostate cancer-associated genes are expressed in a
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from the tissues of various organisms such as humans or other mammals (e.g. mice, sheep and dogs). The methods of the invention are useful for diagnosing and treating prostate cancer in mammals. The prostate cancer-associated genes are useful for diagnosing or treating prostate cancer, as well as for identifying modulators of prostate cancer or agents that inhibit prostate cancer. The nucleic acid sequences are particularly useful in gene therapy, as a vaccine or in antisense applications. ABK92115-ABK92263 represent prostate cancer-associated polynucleotide The present invention relates to methods of detecting a prostate cancerassociated transcript in a cell from a patient. The method comprises
contacting a biological sample from the patient with prostate cancerassociated polynucleotides (designated PC genes) that selectively
hybridise to a sequence that is at least 80% identical to them. The
prostate cancer-associated polynucleotide sequences are differentially
expressed in prostate tumour tissue or in prostate cancer and are derived sequences

Sequence 1195 ВP; 382 A; 221 C; 233 G; 359 T; 0 U; 0 Other;

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                                                                                                                                                Xu J, Dille Kalos MD, 1 Carter D, 1 Mcneill PD, Deng T;
New prostate-specific proteins and genes, useful in gene therapy, particularly for stimulating an immune response in a patient, or prostate cancer in a patient, as well as for diagnosing prostate in a patient.
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29-JUN-2001; 2001US-00895814.
10-DEC-2001; 2001US-00012896.
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MD, Fanger GR, Rette
r D, Li SX, Wang A,
ll PD, Houghton RL, \
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Wang A, Skelky YAW, Hepler WT, Hural J;
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RESULT 12
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                                                                                                                                                         CC The invention relates to newly discovered cancer markers associated with CC the cancerous state of prostate cells. Also disclosed is a method of CC assessing whether a patient is afflicted with prostate cancer. The method cof the invention involves assessing whether a patient is afflicted with prostate cancer by comparing the level of expression of a marker in a CC patient sample and the normal level of expression of the marker in a CC control non-prostate cancer sample, where a significant increase in the CC level of expression of the marker in the patient sample and the normal CC level indicates that the patient is afflicted with prostate cancer. Nucleic acids of the invention are useful for diagnosing or treating CC prostate cancer, and may be useful in gene therapy. Sequences given in CC ADB7517-ADB75631 represent marker cDNA and proteins. Note: The sequence CC data for this patent did not form part of the printed specification, but CC was obtained in electronic format directly from WIPO at CC ftp.wipo.int/pub/published_pct_sequences.
                                     Query Match
Best Local Similarity
Matches 1017; Conserv
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Hoersh S,
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22-AUG-2001; 2001US-0314356P.
25-SEP-2001; 2001US-0325020P.
12-DEC-2001; 2001US-0341746P.
05-MAR-2002; 2002US-0362158P.
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    ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA
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                                                                                                                              382 A;
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onsey AM, Glatt K, Zhao X,
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                                          Score 1017; DB 10;
Pred. No. 2.6e-276;
; Mismatches 0;
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                                                   cDNA; 1195
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480

485 420 425

660 599 600 605 540 545

785 720 725 360

365 300 305 240

1082

1025

18-DEC-2003

(first entry)

prostate specific full length cDNA P789P

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19-MAY-2000;

13-MAY-2000;

13-JUN-2000;

27-JUN-2000;

09-AUG-2000;

06-SEP-2000;

06-SEP-2000;

10-CCT-2000;

10-CCT-2000;

10-CCT-2000;

10-CCT-2000;

10-CCT-2000;

10-DCCT-2001;

10-DEC-2001;
The invention relates to an isolated polypeptide comprising no more than 11-542 amino acids of ADB13563 comprising a sequence ADB14487. The peptides comprise a fragment ADB13563 of that contain naturally processed T-cell epitopes for 3 class I major histocompatibility complex (MHC) alleles. ADB13563 is a polypeptide encoded by a human prostate specific cDNA, one of 648 disclosed as new. Also included are nucleic acids encoding the proteins and peptides, expression vectors, a host cell transformed with the vector, an isolated antibody (or antigen binding fragment) that specifically binds to the protein or peptide, detecting the presence of a cancer in a patient (comprising contacting a patient sample with a binding agent that binds to the peptides or a polypeptide appearing as ADB13558, detecting the amount of polypeptide that binds to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-NOV-1999;
14-JAN-2000;
27-MAR-2000;
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23-SEP-1998;
15-JAN-1999;
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                                                                                                                                                                                                          New isolated polypeptide for use in a vaccine for stimulating an in response, or for treating or diagnosis cancer, preferably prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; ss; prostate specific cDNA; cytostatic; in gene therapy; cell therapy; vaccine; T-cell epitoclass I major histocompatibility complex allele;
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2-NOV-1999;
1-NOV-1999;
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2000US-00685166

2000US-00799729

2000US-00759143

2001US-00780669

2001US-00852911
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99US-00439313.
99US-00443686.
2000US-00483672.
2000US-00558857.
2000US-0055079737.
2000US-0055079737.
2000US-005579737.
2000US-0065783.
2000US-00657279.
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2001US-00012896.
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98US-00159812.
99US-00232149.
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CC comprising the peptides or proteins, stimulating or expanding T cells
CC comprising the peptides or proteins, stimulating or expanding T cells
CC specific for a tumour protein comprising contacting T cells with the
CC peptides or the isolated T cell population, treating prostate cancer in a
CC patient comprising administering a composition comprising the peptides,
CC mucleic acids, antibodies or compounds, determining the presence of a
CC cancer in a patient and treating prostate cancer in a patient comprising
CC from a patient with the peptides or antigen presenting cells that express
CC proliferated T cells to the patient. The peptides (or an oligonucleotide
CC proliferated T cells to the patient. The peptides (or an oligonucleotide
CC presence of cancer in a patient. The peptides, nucleic acids encoding, or
CC stimulate or expand T cells specific for a tumour protein. The peptides,
CC nucleic acids, antibodies, fusion proteins, T cell populations or antigen
CC prostate cancer in a patient. The present sequence is a known cDNA
CC showing sequence similarity to one of the disclosed human prostate
CC specific cDNAs. Note: Except where otherwise indicated, the sequence data
CC obtained in electronic format directly from USPTO at
CC sequence. Supplementation of the printed specification, but was
CC sequence. Attmilled the content of the printed specification, but was
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                                           The present invention relates to a method of prognosticating metastasis in a breast cancer patient involves identifying differential modulation of each gene relative to the expression of the same genes in a normal population in combination of genes. The invention is useful for prognosticating breast cancer in a patient. The present sequence is human STEAP (six transmembrane epithelial antigen of the prostate) DNA used to illustrate the method of the invention
                                                                                                                                                                                                                                                                                                       Prognosticating metastasis in a breast cancer patient comprises identifying differential modulation of each gene relative to the expression of the same genes in a normal population in combination
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Matches 1017
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a method for diagnosing cancer. The method comprising identifying differential modulation of each gene (relative to the expression of the same genes in a normal population) in a combination of genes. The method, diagnostic portfolio and the kit are useful in diagnosing cancer. The method may also be used for determining gene expression profiles. The present sequence is human STBAP (six transmembrane epithelial antigen of the prostate) DNA used to illustrate the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Diagnosing cancer comprises identifying differential modulation of gene (relative to the expression of the same genes in a normal population) in a combination of genes.
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AR371039 Sequence	AR367143 Sequence	AR278447 Sequence	BD242240 Compounds	AC162380 Pan trogl	AC161278 Pan trogl	AC104475 Pan trogl	AC142337 Pan trogl	AC147308 Pan trogl	AC004969 Homo sapi	AC021898 Homo sapi	BC066301 Homo sapi	AY029584 Mus muscu		CQ777614 Sequence	AF297098 Mus muscu	BC061023 Mus muscu	AX155248 Seguence		AR617056 Sequence	AR366784 Sequence	BD232188 Novel ser	AF319659 Sus scrof	CS045211 Sequence	CS040827 Sequence	CS0362S9 Sequence	CS031875 Sequence

ALIGNMENTS

BD232184 Novel serpiginous trans and utilization thereof BD232184 BD232184.1 GI:33041954 D 2002517184-A/1. Homo sapiens (human) Homo sapiens (subsective trans apiens) Homo sapiens (human) Afar, D.E., Hubert, R.S., Morel serpiginous trans and utilization thereof Patent: JP 2002517184-A/1 D 18-JUN-1998 US DANIEL B AFAR, RENE S HU DOUGLAS C SAFFRAN, PC C12N5/10, A61K38/0 PC C12N5/10, A61K38/0 PC C12N5/10, C12P21/0 PC C12N	RESULT 1
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Patent: US 6833438-A 1 21-DEC-2004;
Agensys, Inc.; Santa Monica, CA
Location/Qualifiers
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Afar, D.E., Hubert, R.S.,
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/ Match 100.0%; Score 1017; DB 6; Length 1193; Local Similarity 100.0%; Pred. No. 2.6e-231; 1017; Conservative 0; Mismatches 0; Indels 0; Gaps 0; 1 ATGGAAAGCAGAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 60	/or /db 64. /no /pr /br HLH HLH VVS RRQ YVS RVS ICS	1 Afar,D.B., Hubert,R.S., Raitano,A.B., Saffran,D.C., Mitchell,S.C., Faris,M. and Jakobovite,A. Serpentine transmembrane antigens expressed in human prostate cancers and uses thereof Patent: WO 0140276-A 1 07-JUN-2001; Urogenesys, Inc. (US) Location/Qualifiers 1. 1193	AX155243 Sequence 1 from Patent WOO140276. AX155243 AX155243.1 GI:14536707 Homo sapiens (human) M Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.	904 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCAGAAGATACTCCAACTTT 963 901 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTCGAAGATT 960 901 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 960 904 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGAAGATT 1023 905 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGAAGATACTGAAGATT 1023 906 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAAGATATGTTCCCAGTTG 1017 916 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAAGATATGTTCCCAGTTG 1017	CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAAATGAAGATTTATGTG TCTCTGGGAATTGTGGGAATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT
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CQ776742 1195 bp DNA linear PAT 11-MAR-2004 Sequence 428 from Patent EP1394274. CQ776742.1 GI:45380132 Homo sapiens (human)	781 TCCCTTCTACTGGGACAATACACGCATTGATTTTTGCCTGGATAAGTGGATAGATTAT 840	661 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGACCATCTATTCCATCT 720	484 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGG	TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG	61 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAAGACCAGCATGCTAAAAAGA 120

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/mol_type="unassigned DN/
/db_xref="taxon:9606"
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Pred. No. 2.6e-231;
Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unclassified.
1 (bases 1 to 1195)
Afar,D.E., Hubert,R.S.,
Mitchell,S.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unknown
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GTTTCCATCACTCTTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA
            GTTTCCATCACTCTTTGGCATTGGTTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA
                                                     TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG
                                                                                               ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTTAGCAACT
                                                                                                                             CTTCAGCACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT
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                                                                                                                                                                        CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA
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/mol_type="genomic
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Monica, CA;
            Score 1017; DB 6;
Pred. No. 2.6e-231;
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US 6329503
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Xu,J. Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Xu,J., Dillon,D.C., Mitcham,J.L., Stolk,J.A., Day,C.H.,
Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W.,
Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W.,
Hepler,W.T. and Henderson,R.A.
                                                                                                                        Patent: US 6630305-A 878 07-OCT-2003; Corixa Corporation; Seattle, WA; WOX;
                                                                                                                                                                Compositions and methods
                                                                                                                                                                                                                                      Unknown
                                                                                                                                                                                                                            Unclassified
                                                                                                                                                                                                                                                Unknown
                                                                                                                                                                                                                                                                                                                                                                                          ATGGAAAGCAGAAAAAGACATCACAAAACCAAGAAGAACTTTTGGAAAATGAAGCCTAGGAGA
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                                                                             /organism="unknown"
/mol_type="genomic"
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Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y. Xu,J., Billon,D.C., Mitcham,J.L., Btolk,J.A., Day,C.H. Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H. Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W., Hepler,W.T. and Henderson,R.A.
Compositions and methods for the therapy and diagnosis of
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Corixa Corporation; Seattle, WA
Location/Qualifiers
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Unclassified.
                                                                                                                                                                                                                                                                                                                                                                     Patent: US 6800746-A 878 05-OCT-2004; Corixa Corporation; Seattle, WA
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GTTTCCATCACTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA
                     TCCCATCAACAATATTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG
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Query Match Best Local Similarity 100.0%; Pro Matches 1017; Conservative 0; 1 Qy 1 ATGGAAAGCAGAAAAGACATCACJ Db 66 ATGGAAAGCAGAAAAGACATCACJ	JOURNAL Patent: US 6887975. Al 103-MAY- Agensys, Inc.; Santa Monica, C FEATURES Location/Qualifiers Source /organism="unknown" /mol_type="genomic DN ORIGIN	NISM Unknown. Unclassified. Unclassified. NCE 1 (bases 1 to 1195) ORS Afar, D.E., Hubert, R.S., Mitchell, S.C.	LOCUS AR654075 1199 DEFINITION Sequence 1 from patent US 67 ACCESSION AR654075 VERSION AR654075.1 GI:67584962 KEYWORDS Unknown.	SULT 9	961 AGA	901	841	Qy 781 TCCCTTCTACTGGGCACAATACA	Oy 721 GTGAGTGACTCTTTGACATGGAG	Qy 661 TCTCTGGGAATTGTGGGATTGGCAATA	666	Db 606 TCTTACCCAATGAGGCGATCCTG	Db 546 AGAAAGCAGTTTGGGCTTCTCAG OY 541 TCTTACCCAATGAGGCGATCCTA	481	Qy 421 CTTCATAATGGAACCAAGTATAA	426
100.0%; Score 1017; DB 6; Length 1195; imilarity 100.0%; Pred. No. 2.6e-231; Gaps 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0; ATGGAAAGCAGAAAGCAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 60	AY-200 , CA , CA DNA"	Leong, K., Raitano, A.B., Saffran, D.C. and	195 bp DNA linear PAT 13-JUN-2005 6887975.	CHANNIT THE CHANNET CANADA THE TOTAL CHANNET OF THE	GICCIGALAIIIAAAAAGCAIACIAIICCIGCCAIGCITGAGGAAGAAGAAGAIACIGAAGAATT 1025 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1017	CARCIIIAIGAIAGCIGITITCCTTCCAATTGIT 9 TCCTGCCATGCTTGAGGAAGAAAATT 9		TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATA	TGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 780 	CTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 720 	CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 725	0	TTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 605	AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCA	CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGG	485
RESULT 10 AX201105 LOCUS DEFINITION ACCESSION VERSION KEYWORDS	p	B & 8	D & B (S B 8	, p 4	g da	- B 49	S B	Qy B	Db Qy	<i>S</i> 8	\$ 8	Db Qy	ממ	δ B	Qy
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CORPORATION (US)
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent: WO 0173032-A 878 04-OCT-2001; CORIXA CORPORATION (US)
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Query Match 100.0%; Score 1017; DB 6; Length 1195;	/organism="nomo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606" ORIGIN	rce	Patent: EP 1355150-A 35 22-OCT-2003; Ortho-Clinical Diagnostics, Inc. (US) Location/Qualifiers	REFERENCE 1 AUTHORS Wang, Y. TITLE Panel of nucleic acid sequences for cancer diagnosis	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.	Homo sapiens (human) Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebra		DEFINITION Sequence 35 from Patent BP1355150. ACCESSION AN905483	183 AV026402 1105 hp TWD 12-02-4 TAT 10-	Qy 961 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1017	Db 966 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 1025	QY 901 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 960	Qy 841 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCC	Qy 781 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATA	Qy 721 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 780	Qy 661 TCTCTGGGAATTGTGGCATTGGCTGTTGGCTGTTGGCTGTTGTTGTTTCCATCT 720	Qy 601 CAACAAAATAAAGAAGATGCCTTGGATTTGAGCATGATGTTTGGAGAATTTATGTG 660	Qy 541 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 600	QY 481 AGAAAGCAGTITGGGCTICTCAGTTTCTTTTTTGCTGTACTGCATGCAAITTATAGTCTG 540	Qy 421 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGG	ű ö	366
RESULT 13	Db 1026 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1082		OY 901 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 960	Db 906 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCC	QY 841 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCC	QY 781 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATA	Db 786 GTGAGTGACTCTTTGACATGGAGAGAATTTTCACTATATTCAGAGCTAGGAATTGTT 845	Qy 721 GTGAGTGACTCTTTGACATGGAGAAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 780	OY 661 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 720	Qy 601 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 660	Db 606 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 665	QY 541 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 600	OY 481 AGAAAGCAGTTTGGGCTTCTCAGTTTTTTTTGCTGTATCTGCAATTTATAGTCTG 540	OY 421 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGG	Oy 361 GITTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 420	OY 301 TCCCATCAACAATATTTTATAAAATTCCAATCCTGGTCATCAACAAGTCTTGCCAATG 360	OY 241 ATAGCATCTCTGACTTTTTTTTTACACTCTTTTGGGGAAGTAATTCACCCTTTAGCAACT 300	OY 181 CTTCAGCACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 240	OY 121 CCTGTGCTTTTGCACTAACAGCCCATGCTGATGAATTGACTGCCCTTCAGAA 180	OY 61 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 120	Qy 1 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 60	Best Local Similarity 100.0%; Pred. No. 2.6e-231; Matches 1017; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Hominidae; Homo.
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Location/Qualifiers
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                                                                                                            100.0%; Silarity 100.0%; IConservative 0;
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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                       CTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT
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Pred. No. 2.6e-231;
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                                                            1 (bases 1 to 1195)

Hubert,R.S., Vivanco,I., Chen,E., Rastegar,S., I
Mitchell,S.C., Madraswala,R., Zhou,Y., Kuo,J., R
Jakobovits,A., Saffran,D.C. and Afar,D.E.
STEAP: a prostate-specific cell-surface antigen
human prostate tumors
Proc. Natl. Acad. Sci. U.S.A. 96 (25), 14523-145
2 (bases 1 to 1195)
Hubert, R.S., Vivanco, I., Chen, E., Rastegar, S., Mitchell, S.C., Madraswala, R., Zhou, Y., Kuo, J., Jakobovits, A., Saffran, D.C. and Afar, D.E.H.
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42.2	42.6	43.1	43.5	44.8	45.2	45.3	45.3	45.4	45.7	46.5	46.6	47.7	48.1	48.6	49.3	49.4	50.3	51.1	51.3	51.3	52.8	52.9
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ALIGNMENTS

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AVA03218	1050 bp DNA linear GSS	Locus
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Best Local Similarity 99.9%; Pred. No. 1.3e-259; Matches 1016; Conservative 0; Mismatches 1;

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CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT

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CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA

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KEYWORDS
SOURCE
ORGANISM
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Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and order
them based on alignment.
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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M. Tier from human chirp mouse orthology.
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ilarity 89.2%;
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/mol_type="genomic DNA"
/db_xref="taxon:9598"
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AGENCOURT 10807821 MAPCL H
mRNA sequence.
CA488012
CA488012.1 GI:24948800
EST.
                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
Email: Cgapbs-r@mail.nih.gov
Tissue Procurement: Kristi A. Egland, Ira Pastan
CDNA Library Preparation: Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                    Hominidae; Homo.

1 (bases 1 to 884)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection
Unpublished (1999)
                                                                                            found through the I.M.A.G.E. Consortium/LLNL
http://image.llnl.gov
Plate: LLAM14278 row: c column: 10
High quality sequence stop: 758.
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Mammalia; Eutheria;
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6719746"
                                                                           Location/Qualifiers
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Homo
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b sapiens cDNA clone IMAGE:6719746 5',
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/rote="Vector: pCMV-SPORT6; Site 1: EcoRV; Site 2: Not 1;
/note="Vector: pCMV-SPORT6; Site 1: EcoRV; Site 2: Not 1;
Subtracted with brain, liver, lung, kidney and muscle.
Subtracted with brain, liver, lung, kidney and muscle.
Directionally cloned. Priming method: oligo-dT. Average insert size: 1800 bp. Library amplification: 26,000 fold.
Kristi A. Egland, James J. Vincent, Robert Strausberg,
Bungkook Lee & Ira Pastan: Discovery of new breast cancer genes encoding membrane and secreted proteins.
Manuscript submitted."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /cell_line="ZR-75-1,
hTERT-HME1, LNCaP"
/lab_host="EMDH10B"
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99.4%;
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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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This sequence was ma
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    GTTTCCATCACTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA
                                                TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG
                                                                                                       ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGGAAGTAATTCACCCTTTAGCAACT
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/mol_type="genomic DNA"
/db_xref="taxon:10090"
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/locus_tag="HCM1484"
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Shibata, K.,
Konno, H., Ar
                                                       Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                             Carninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA Meth. Enzymol. 303, 19-44 (1999) 10349636
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AK010437.1 GI:12845880
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  ., Itoh, M., Aizawa, K., Akiyama, J., Nishi, K.,
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Mus musculus ES cells cDNA, RIKEN full-length enriched library, clone:2410007B19 product:six transmembrane epithelial antigen of the prostate, full insert sequence. Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Bukaryota; Metheria; Euarchontoglires; Glires; Rodent
Mammalia; Eutheria; Euarchontoglires; Glires; Rodent
Sciurognathi; Muridae; Murinae; Mus. Rodentia; Euteleostomi;

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18 (bases 1 to 1211)

18 Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H., Adachi, J., Aizawa, K., Akahira, S., Fukuda, S., Fukunishi, Y., Adachi, J., Bono, H., Carninci, P., Fukuda, N., Hiramoto, K., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Itoh, M., Izawa, M., Hiraoka, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Saito, H., Saito, H., Sakkai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Shibata, K., Shibata, Y., Tagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yasunishi, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y., Toshini, Sano, T., Takahashi, F., Tanaka, T., Toya, T., Takahashi, F., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yasunishi, A., Yoshida, K., Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                     Submitted (10-UUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (B-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
Please visit our web site (http://genome.gsc.riken.jp/) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,B., Watshiki,M.; Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y., RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Group Phase I & II Team. Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
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                                                                                                                                                                                    /organism="Mus musculus"
/mol type="mRNA"
/strain="C57BL/6J"
/db_xref="FANTOM_DB:2410007B19"
/db_xref="taxon:10090"
/clone="2410007B19"
/coll_type="ES_cells"
/codon_start=1
/proteIn_id="BA
/db_xref="GI:12
                                                                               /note="unnamed protein product; putative six transmembrane epithelial antigen of the prostate (MGD|MGI:1917608, GB|AK010437, evidence: BLASTN, 100%
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                                                                                            GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT
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TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT
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HLQHAVHVDAFDCPSELQHTQBEFPNWRLPVKVAAIISSITFLYTLLREIIYBLUTSR
EQYFYKIFILVINKVLPMVAITLLALYYLPGELAAVVQLKRGTKYKKFPPWLDRWMLA
KKQFGLLSFFEAVLHAYYSLSYPMRRSYRYKLLNWAYKQVQQNKEDAWVEHDVWRWEI
YVSLGIVGLAILALLAVTSIPSVSDSLTWREFHYIQSKLGIVSLLLGTVHALVFAWNK
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82.8%;
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Pred. No. 2.7e-185;
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Qy 186 GCACACAGAGAACTCT Db 1 GCACACACAGAACTCT	Ouery Match Query Match Best Local Similarity 93.6%; Matches 777; Conservative		/organism="Homo /mol_type="mRNA; /db_xref="caxon: /clone="IMAGE:4" /lab_host="DH10! /clone_lib="NIH] /note="Organ: li Sfil (ggccgcctcg 3' adaptors were	Plate: LLCM1549 row: b column: High quality sequence stop: 704. PEATURES Location/Qualifiers source 1.881	DNA Sequencing by: Clone distribution found through the I http://image.llnl.go	Email: cgapbs-r@mai Tissue Procurement: cDNA Library Prepa: cDNA Library Array	AUTHORS NIH-MGC http://mgc.nci.nih.gov/. TITLE National Institutes of Health, M JOURNAL Unpublished (1999) COMMENT Contact: Robert Strausberg, Ph.D	•	3	LOCUS B6565247 DEFINITION 602582917F1 NIH_MGC_ mRNA sequence. ACCESSION B6565247	RESULT 6 BG565247	Qy 961 AGACATGGTTGGGAAGAQ 	Qy 901 GTCCTGATATTTAAAAGG	Qy 841 AAACAATTTGTATGGTAT
GCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATTATAGC		5'-ATTCTAGAGGCGAGGGGGGCGAAATG-dT (30)BN-3' (where B = A), C, or G and N = A, C, G, or T). Average insert size 1.85 kb (range 1.0-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."	organism="Homo sapiens" mol_type="mRNA" db_xref="taxon:9606" clone="IMAGE:4710436" lab host="DH10B (T1 phage-resistant)" lab host="DH10B (T2 phage-resistant)" clone_lib="NIH MGC_76" note="Organ: liver; Vector: pDNR-LIB (Clontech); Site fil (ggccgcctcggcc); Site 2: Sfil (ggccattatggcc); 5', daptors were used in cloning as follows: 5', daptor	7: b column: 05 :e stop: 704. walifiers	DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov	<pre>cgapbs-r@mail.nih.gov procurement: CLONETECH Laboratories, Inc. Library Preparation: CLONETECH Laboratories, Inc. Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)</pre>	<pre>ngc.nci.nih.gov/. ites of Health, Mammalian Gene Collection (MGC) 99) Strausberg, Ph.D.</pre>	Chordata; Craniata; Vertebrata; Euteleostomi; Euarchontoglires; Primates; Catarrhini;	900	881 bp mRNA linear EST 10-APR-2001 602582917F1 NIH_MGC_76 Homo sapiens cDNA clone IMAGE:4710436 5', mRNA sequence. BG565247		AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1017	GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 9	AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCC
245 JOHN 60 COMMENT 305	S; REFERENCE AUTHORS		Qy Db Db RESULT 7 and BE875216 LCCC DEFINITION	Oy Ob	Qy Db	Qу	Qy Db		Oy Oy	2001 Qy	Qy Db	Qy Db	960 Qy 1057 Db	900 Qy 997 Db
AL Unpublished (1999) Contact: Robert Strausberg, Ph Email: cgapbs-r@mail.nih.gov Tissue Procurement: DCTP/DTP/G cDNA Library Preparation: Lif cDNA Library Arrayed by: The DNA Sequencing by: Incyte Gen Clone distribution: MGC clone	Ammmalia, Butheria; Buarchontoglires; Primates; Cata Hominidae; Homo. 1 (bases 1 to 710) NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collect	mRNA sequence. BE875216 BE875216.1 GI:10323992 EST. Homo sapiens (human) Homo sapiens (human)	961 AGACATGGTTGGGAAGACGTCACCAAAATTAACCAAAACTGAGATATGTTC 1010	904 CTGATATTT-AAAAGCATACTATT-CCTGCCATGCTTGAGGAAGAAGATACT-GAAGATT 960 	844 CAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCC	786 TCTACTGGGCACAATACACGCATTGATTTTTTGCCTGGAATAAGTGGATAGATATAAAA 843	726 TGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCTAGGAATGGTATCCCT 785			546 CCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTCCAACA 605	486 GCAGITTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTGTCT	426 TAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACAAGAAA 485	366 CATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAACTTCA 425	306 TCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATGGTTTC 365

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Plate: LLAM9674 row: p column:
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                           GTCTCTGGGAATTGTGGGATTGG 682
                                                                         CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTTGGAGAATGG-AGATTTATGT
                                                                                                                                   TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC
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                                                       CAACAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGCAGATTTATGT
                                                                                                                  TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC
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/tissue_pe="large_cell carcinoma, undifferentiated"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_69"
/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.1 kb. Library constructed by Life Technologies."
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/mol_type="mRNA"
/db_xref≃"taxon:9606"
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Pred. No. 2.2e-162;
0; Mismatches 5;
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RESULT

(http://genome.uiowa.edu/pubsoft/software.html) present in

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Prather, R.S., Antoniou, B., Garverick, H.A., Green, J.A., Poetter, R.S., Matth, M.F. and Youngquist, R.S.
USDA Grant NRI-2002-03476: Bovine ESTs: Focus on Female
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Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
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Library construction (Standard Protocol): All procedures have been described in detail elsewhere (Soares et al., 1994; Bonaldo et al., 1996; Jiang et al., 2001). Total cellular RNA from each sample was isolated by using STAT-60 reagent (Tel-Test, Friendswood, TX) and the poly(A)+ RNA was obtained by two rounds of purification with the Oligotex mRNA isolation kit (Qiagen) according to the manufacturer's instructions. The libraries were constructed essentially as described by the manufacturer's instructions provided with the SuperScript Plasmid System (Invitrogen, cat. no. 18248-013). Briefly, Imcg of poly(A)+ RNA was annealed at c37 degrees with 10mcg of NotI-tag-dr18 oligonucleotide (GCTGCTGCGGCCGC-tag-T18) and reverse transcribed at c37 degrees with SuperScript II (Invitrogen) reverse transcriptase (Jiang et al., 2001). The 'tag' represents a tissue/stage-specific ten-base sequence identifier
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               selected and preovulatory); oviduct (days 0, 3 and 5); endometrium (days 5, 8, 14, 16, 18 and 35); and placenta/embryo from day 35 conceptuses. Expanded descriptions of how the tissues were collected can be found at the following URL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            while not registered have known Angus pedigrees going bac at least 4 generations. Samples collected: The samples consisted of the following: germinal vesicle-stage occytes; in vitro derived embryos (2-cell, morula, blastocyst and nuclear transfer blastocyst; in vivo blastocysts and conceptuses (days 8, 14, 16 and 18); corpora lutea (days 3, 5, 8, 14, 16, 18 and 35); ovarian follicles (days 0, non-recruited, recruited, early selected and propolatory), ovident days 0, 1 and 5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Reproduction' to RS Prather(Primary Investigator), E Antoniou, HA Garverick, JA Green, MC Lucy, RM Roberts, Smith and RS Youngquist. Genetic Source: Heifers for the project were purchased from Circle A Ranch, Iberia, MO (http://www.circlearanch.com/home.html). These heifers, the project was circlearanch.com/home.html).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           http://genome.rnet.missouri.edu/Bovine/Methods.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Vector: pSport1; Funding: The production of ESTs submitted in this project was funded by USDA Grant MRI-2002-03476 entitled 'Boyine ESTs: Focus on Female
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Bos taurus"
/mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the oligonucleotide used to prime first-strand synthesis. Second strand synthesis was performed with T4 DNA polymerase in the presence of DNA ligase and RNase H. After second strand synthesis, the double-stranded cDNAs were ligated to Sall adapters (Invitrogen-Life Technologies) and digested with NotI. The cDNAs were size selected by passage through cDNAs ize fractionation columns (Invitrogen-Life technologies). The cDNAs derived from each developmental stage of a particular tissue were mixed on an equimolar basis and ligated directionally into
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        contain long poly(dA) tails. Biotechniques 31:38-42. Soares MB, MF Banaldo, P Jelene, L Su, L Lawton, A Efstrantiadds. 1994. Construction and characterization a normalized cDNA library. Proc Natl Acad Sci,
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National Institutes of Health, M
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Mammalia; Eutheria;
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Tissue Procurement: ATCC/DCTD/DTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 961)
                                                                                                                                                                                                                                                                                             quality sequence stop:
/tissue_type="melianotic melanoma, high MDR (cell line)"
/lab_host="DH10B (phage-resistant)"
/clone lib="NIH MGC_49"
/clone lib="NIH MGC_49"
/note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
ECCRI; cDNA made by oligo-dT priming. DIrectionally cloned
into EccRI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
                                                                                                                                                                                             /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                               clone="IMAGE:4858820"
                                                                                                                                                                                                                                       organism="Homo sapiens"
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Best Local Similarity 93.1%;
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BG182296
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Homo sapiens (human)
Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Library.
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0; Mismatches
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216 431 9900
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Hominidae; Homo.

1 (bases 1 to 796)

1 (cain, S., Leventhal, C., Thornton, M., Ramachandran, R., Whittington, J., Lerner, L., Costanzo, D., McElligott, K., Boozmays, R., Smith, E., Veloso, N., Klika, A., Hess, J., Cothren, K. Offenbacher, J., Danzig, J. and Ducar, M. Creation of genome-wide protein expression libraries using activation of gene expression

Nat. Biotechnol. 19 (5), 440-445 (2001)
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GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /ceTl_line="HT1080"
/clone lib="Athersys RAGE Library"
/clone lib="Athersys RAGE Library"
/clone lib="Athersys RAGE Library"
/note="See 'Creation of Genome-wide Protein Expression
Libraries using Random Activation of Gene Expression',
Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Pred. No. 8.3e-152;
0; Mismatches 17;
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Cothren,K., I
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Email: cgapbs r@mail.nih.gov

Tissue Procurement: Dr. Jose Mercuende

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@ulowa.edu
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1 (bases 1 to 720)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
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UI-H-ED1-axr-o-23-0-UI 3', mRNA sequence.
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                                Conservative
                                                                                                                                                                                                                                 /clone lib="NCI CGAP ED1"
//clone lib="NCI CGAP ED1"
//note="Organ: Left Pubic Bone; Vector: pT7T3-Pac
(Pharmacia) with a modified polylinker; Site 1: EcoR I;
Site 2: Not I; NCI CGAP ED1 is a normalized cDNA library
containing the following tissue(s): Chondrosarcoma cell
line CS5. The library was constructed according to
Bonaldo, Lemnon and Soares, Genome Research, 6:791-806,
1996. First strand cDNA synthesis was primed with an
oligo-dT primer containing a Not I site. Double stranded
cDNA was ligated to an EcoR I adaptor, digested with Not
I, and cloned directionally into pT7T3-Pac vector. The
oligonucleotide used to prime the synthesis of
first strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tag for this library is GCTCAAGGCT.
                                                                                                                                                                               TAG_TISSUE=chondrosarcoma
TAG_LIB=UI-H-ED1
TAG_SEQ=CGTCAAGGCT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="Chondrosarcoma"
/dev_stage="Adult"
/lab_host="DH10B_(Life_Technologies)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-ED1-axr-o-23-0-UI"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Homo sapiens"
                                                                                              59.5%;
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                                                                              0;
                                                                           Score 605.4; DB 6;
Pred. No. 3.3e-150;
0; Mismatches 1;
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Tomarev,S.I., Wistow,G., Raymond,V., Dubois,S. and Mal Gene expression profile of the human trabecular meshwo sequence tag analysis
Invest. Ophthalmol. Vis. Sci. 44 (6), 2588-2596 (2003)
                                                      Email: graeme@helix.nih.gov
Plate: 24 row: h column:
Seq primer: M13RP1 reverse |
                                                                                                                      Tel: 301 402 3452
Fax: 301 496 0078
                                                                                                                                                          Section on Molecular Structure and Function
National Eye Institute
6/331, NIH, Bethesda, MD 20892-2740, USA
                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (human)
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                                                                                                                                                                                                                           Contact: Wistow G
                                                                                                                                                                                                                                                                                                                                                                    Hominidae; Homo.
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                                   Location/Qualifiers
organism="Homo sapiens"/
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Matches 609; Conserv
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/note="Organ: Eye; Vector: pSPORTI; The cDNA,
directionally cloned in the pSPORTI vector (Life
Technologies, Rockville, MD), was constructed at Bioserve
Biotechnology (Laurel, MD) essentially following the
protocols of the SuperScript Plasmid System full details
of which are contained in the manufacturer's Instruction
manual (http://www.lifetech.com/). Sublibraries
(designated ho, hp, and hq) were made from the first three
35-uL fractions of cDNA from a Sephacryl S-500 HR resin
column. EST analysis was performed on the unamplified
library at the NIH Intramural Sequencing Center(NISC)."
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/db_xref="taxon:9606"
/clone="ho24h02"
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/dev_stage="Adult"
/lab_host="EMDH10B"
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Pred. No. 3e-148;
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                                                                                                                                                                                                                                                                         100 ÁTGGAÁAGCAGAAAAGACATCACAAACCAAGAAGAACTTTTGGAAAAATGAAGCCTAGGAGA
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1 (bases 1 to 697)

1 (bases 1 to 697)

Birkett,C., Cho,J., Gau,Y., Hamer,R., Kelly,S., Kovacs,K., Liu,L.

Liu,X., Porter,J., Sachs,A., Shu,Y., Sun,Z., Wong,J., Wu,M.,

Zhang,X., Jay,G. and He,W.

High-throughput cloning of full-length human cDNAs directly from chun libraries optimized for large and rare transcripts
                                                                                                                                                                                                                                                                                                                   1 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished Contact: Kovacs, KF
Contact: Kovacs, KF
High Throughput cDNA Cloning
High Throughput cDNA Cloning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This EST submission is part of an on-going human full-length cloning project at OriGene Technologies, Inc. Please contact OriGene for access.
OriGene Technologies, Inc.
6 Taft Ct. Suite 100
Rockville, MD 20850
Tel: (301) 340-3188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OriGene Technologies, Inc. ( www.origene.com
6 Taft Court, Suite 100, Rockville, MD 20850,
Tel: 301 340 3188
Fax: 301 340 8606
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                                                                                                                                                                                                                                                                                                                                              h 58.8%; Score 598; DB 8; Los Similarity 100.0%; Pred. No. 3.1e-148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      http://www.origene.com
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                                                                                                             CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA
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/clone_Tib="Human breast cancer tissue, large insert, pCN
/clone_Tib="Human breast cancer tissue, large insert, pCN
/clone_Tib="Human breast cancer tissue); Vector:
/note="Organ: Mammary gland (cancer tissue); Vector:
pCNV6-XL5; Site 1: EcoR1; Site 2: Xho1/Sall compatible er
ligatio; Oligo-dT primed reverse transcription optimized
for large and GC rich mRNA transcripts, CDNA size
selection, optimized ligation for large inserts into
mammalian expression vector, random clones selected for
end sequence verification of full-length genes"
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/db_xref="taxon:9606"
/clone="TC115356"
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                              724;
mRNA sequence.
BE881257
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Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAN9684 row: k column: 10
High quality sequence stop: 732.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                 Tissue Procurement: DCTD/DTP/Gazdar
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
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601492338F1 NIH_MGC_69 Homo
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BST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
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1 (bases 1 to 920)
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                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cgapbs-r@mail.nih.gov
                                                                                                       /clone="IMAGE:3894657"
/tissue type="large cell carcinoma, undifferentiated"
/lab host="DH108 (phage-resistant)"
/clone_lib="NH1M_MGC_69"
/note="Organ: lung; Vector: pCMV-SPORT6; Site 1: NotI Site_2: Sall; Cloned unidirectionally. Primer: Oligo Average insert size 1.1 kb. Library constructed by Technologies."
                                                                                                                                                                                                                                      /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                             58.8%;
                              0;
                            Score 597.8; DB 2;
Pred. No. 3.7e-148;
0; Mismatches 37;
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AGENCOURT 41384224 NIH MGC 278 Homo
IMAGE:7772991 3', mRNA sequence.
Contact: Daniela S. Gerhard, Ph
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20
                                                                              Hominidae; Homo.
1 (bases 1 to 742)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, 1
                                                               Unpublished (1999)
                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAACTTCATAATGGAACCAA
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Tissue Procurement: Meri Firpo
cDNA Library Preparation: Express Genomics
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM15916 row: h column: 13
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                                                     GTTTCCATCACTCTTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="pluripotent cell line derived from blastocyst inner cell mass"
/lab_host="PH10B TonA"
/clone_lib="NH1 MGC_278"
/clone_lib="NH1 MGC_278"
/clone_lib="NH1 MGC_278"
/clone_lib="NH1 MGC_278"
/clone_lib="NH1 MGC_278"
/clone_lib="NH1 MGC_278"
/note="Grgan: Blastocyst; Vector: pExpress-1; Site_1:
ECORV; Site_2: NotI; RNA obtained from pluripotent cell
line derived from blastocyst inner cell mass (cell line
HSF-1.14, NH Registry designation UC01. Positive for OCT4
expression by rtPCR, positive for SSEA-3, SSEA-4,
Tra-1-80 by immunofluorescence. Negative for
SSEA-1 by immunofluorescence. Passage 35. This line is a
subclone of the parental line; the parental line was
subcloned to remove aneuploid cells). cDNA was primed
using oligo-dT primer:
subcloned to remove aneuploid cells). cDNA was primed
using oligo-dT primer:
5'-pGACTAGTTCTAGATCGCGACCGCCCC(T)25-3' and cloned into
the ECORV/NotI sites of pExpress-1. Size-selection >1.25
kb resulted in an average insert size of 1.9 kb. This
primary library is non-normalized (normalized primary
library is NIH MGC_279) and was constructed by Express
Collection library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Homo sapiens"
mol_type="mRNA"
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Pred. No. 1.1e-147;
0; Mismatches 15; Indels
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